

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 13:38:07 ; Search time 3280 Seconds  
(without alignments)  
3362.794 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1992

Sequence: 1 MKEYVLLFLALCSAKPFFS.....PATFRCVLSRMSVQLNGFM 379

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Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Fgapext 7.0  
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Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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9	1517	76.2	2089	9	AK027359 Homo sapi
10	1385	69.5	1903	9	AK000136 Homo sapi
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13	1040.5	52.2	1107	6	A77048 Sequence 1
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39	969	48.6	1618	5	GDDECORIN
40	967	48.5	1492	4	AF125537 Sus scrofa
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# ALIGNMENTS

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DEFINITION AF316824  
ACCESSION AF316824  
VERSION AF316824.1 GI:13625796  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1184)  
AUTHORS Lorenzo, P., Aspegberg, A., Omnerfjord, P., Bayliss, M.T., Neame, P.J. and Heinemann, D.  
TITLE Identification and characterization of asporin, a novel member of the leucine-rich repeat protein family closely related to decorin and biglycan  
JOURNAL J. Biol. Chem. 276 (15), 12201-12211 (2001)  
MEDLINE 21192276  
PUBMED 11152692  
REFERENCE 2 (bases 1 to 1184)  
AUTHORS Aspegberg, A.  
TITLE Direct Submission  
JOURNAL Submitted (26-OCT-2000) Cell and Molecular Biology, Lund University, BMC plan C12, Lund SE-221 84, Sweden  
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Score: 1992.00 Length: 1184 Matches: 379

Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
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QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetClnAspThrAspAsp 40  
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QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
Db 139 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 198  
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QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleGlyGluIleLysGluAsnAsp 120  
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QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140  
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QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160  
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QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
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QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280  
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Db 919 AAAAAAATCCCTTCAGGATTACAGAGTTGAAATACCTCCAGATATATCTTCTTCTTCT 978  
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Db 1039 TCTTTATACAGTCAATAGTTATTATCAACACCCCGTGAATACCTGGGAATGCAACCT 1098
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1099 GCACACATTCCTGTGTGTTTGACGACAGTGGTTTCAGCTTGGGAACCTTGGAAATG 1155

RESULT 2
AX400320 2454 bp DNA linear PAT 06-JUN-2002
LOCUS
DEFINITION
Sequence 1 from Patent EP1191101.
ACCESSION
AX400320
VERSION
AX400320.1 GI:21336501
WORDS
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Baker, K.P., Chen, J., Goddard, A., Gurney, A.L., Wood, W.I. and Yuan, J.
Polypeptides and nucleic acids encoding the same
Patent: EP 1191101-A 1 27-MAR-2002;
Genentech, Inc. (US)
FEATURES
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BASE COUNT 835 a 432 c 417 g 770 t
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Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0

US-09-944-884-2 (1-379) x AX400320 (1-2454)

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QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
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QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120
534 TTTGATACCTGAATGCTTGATCTTCAAAACAATAAATAAGGAAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
594 TTTAAGAGACTCACTTCTACCTTTATGCTGATCTGATCTGATCTGATCTGATCTGATCTGAT 653
QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160

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Db 714 CTAAGTGAATACCACTTAATCTTCCCAATCATTAGCAGACTCAGAAATTCATGAAAT 773
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LOCUS
DEFINITION
Sequence 29 from Patent WO0208284.
ACCESSION
AX454444
VERSION
AX454444.1 GI:21713846
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human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Pao, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.N., Wood, W.I.
and Ye, W.
Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis
Patent: WO 0208284-A 29 31-JAN-2002;
Genentech, Inc. (US); Baker, Kevin-P. (US); Ferrara, Napoleone
(US); Gerber, Hanspeter (US); Gerritsen, Mary E. (US); Goddard,
Audrey (US); Godowski, Paul J. (US); Gurney, Austin L. (US);
Hillan, Kenneth J. (US); Marsters, Scott A. (US); Pan, James (US);
Pao, Nicholas F. (US); Stephan, Jean-Philippe F. (US);
Watanabe, Colin K. (US); Williams, P. Mickey (US); Wood, William
I. (US)
FEATURES
Location/Qualifiers

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/db\_xref="taxon:9606"  
BASE COUNT 835 a 432 c 417 g 770 t  
ORIGIN

Alignment Scores:  
Pred. No.: 3.1e-166 Length: 2454  
Score: 1992.00 Matches: 379  
Percent Similarity: 100.00% Conservativeness: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
DB 294 CCTTCACATCGCAGTGAATATGATGCTGAGGATATGAGGATATGAGGATATGAGGAT 353

QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
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QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80  
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QY 81 TyrSerArgValIleHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100  
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DEFINITION  
ACCESSION  
VERSION  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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Baker, K.P., Ferrara, N., Gerber, H., Gritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,

Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
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Patent: WO 0200690-A 29 03-JAN-2002;  
Genentech, Inc. (US)  
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DEFINITION		Homo sapiens periodontal ligament associated protein 1 (PLAP1)	
ACCESSION	AY029191	mRNA, complete cds.	
VERSION	AY029191.1	GI:16151084	
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REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	
TITLE		1 (bases 1 to 2466)	
JOURNAL		Yamada, S., Murakami, S., Matoba, R., Ozawa, Y., Yokokoji, T.,	
MEDLINE		Nakahira, Y., Ikezawa, K., Takayama, S., Matsubara, K. and Okada, H.	
PUBMED		Expression profile of active genes in human periodontal ligament	
REFERENCE		and isolation of PLAP-1, a novel SLRP family gene	
AUTHORS		Gene 275 (2), 279-286 (2001)	
TITLE		2 (bases 1 to 2466)	
JOURNAL		Yamada, S., Murakami, S., Matoba, R., Matsubara, K. and Okada, H.	
MEDLINE		Direct Submission	
PUBMED		Submitted (03-APR-2001) Department of Periodontology, Osaka	
REFERENCE		University Graduate School of Dentistry, 1-8 Yamadaoka, Suita,	
AUTHORS		Osaka 565-0871, Japan	
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 Strausberg, R.  
 Direct Submission  
 Submitted (29-JUL-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Marcello Bento Soares, Ph.D.  
 cDNA Library Preparation: Soares Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
[info@bcsc.bc.ca](mailto:info@bcsc.bc.ca)  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
 Ness, Pawan Pandoh, Anna-Lilisa Prabhu, Parvaneh Saeedi, Jacqueline  
 Schein, Duane Smalls, Michael Smith, Lorraine Spence, Jeff Stott,  
 Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyderduyn, Marco Marra.  
 Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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RESULT 9  
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 AK027359  
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 CE oligo capping: fis (full insert sequence).  
 CE Homo sapiens embryo, 10 weeks whole embryo, mainly body cDNA to  
 mRNA, clone\_lib:HEMBB1 clone:HEMBB1001871.

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1  
 AUTHORS Isoqai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y.,  
 Nishikawa, T., Nagai, K., Sugano, S., Shiratori, A., Sudo, H.,  
 Wagatsuma, M., Hosoi, T., Kaku, Y., Kodaira, H., Kondo, H.,  
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 Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K.,  
 Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A.,  
 Nakamura, Y., Nagahara, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T.  
 NEDO human cDNA sequencing project

TITLE Unpublished  
 JOURNAL 2 (bases 1 to 2089)  
 REFERENCE Isoqai, T. and Otsuki, T.  
 AUTHORS Direct Submission  
 TITLE Submitted (10-MAY-2001) Takao Isoqai, Helix Research Institute,  
 Genomics Laboratory, 1533-3 Yana, Kisarazu, Chiba 292-0812, Japan  
 JOURNAL (E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)  
 NEDO human cDNA sequencing project supported by Ministry of  
 Economy, Trade and Industry of Japan; cDNA full insert sequencing;  
 Research Association for Biotechnology; cDNA library construction;  
 5'- & 3'- end one pass sequencing and clone selection; Helix  
 Research Institute (supported by Japan Key Technology Center etc.)  
 and Department of Virology, Institute of Medical Science,  
 University of Tokyo.

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US-09-944-884-2 (1-379) x AK027359 (1-2089)

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## RESULT 10

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ACCESSION AK000136
VERSION AK000136.1 GI:7020026
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SOURCE Homo sapiens colon cDNA to mRNA, clone_lib:COL clone:COL06190.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
THORS Kawabata,A., Hikiiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
Unpublished
REFERENCE 2 (bases 1 to 1903)
THORS Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
JOURNAL Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Department of Virology; Shirokane-dai, 4-6-1,
Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp,
Tel:81-3-5449-5286, Fax:81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry for Biotechnology; cDNA library
sequencing; Research Association for Biotechnology; Department of
construction, 5'- 3'-end one pass sequencing; Department of
Virology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
Agency).
FEATURES
source Location/Qualifiers
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 69.53% Indels: 0
DB: 9 Gaps: 0
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RESULT 13
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DEFINITION Sequence 1 from Patent EP0686397.
ACCESSION A77048
VERSION A77048.1 GI:6088837
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Koops, A. and Hasenoehl, R.D.
TITLE USE OF CHONDROITIN SULPHATE PROTEOGLYCAN FOR PROTECTION OF NEURONS
JOURNAL Patent: EP 0686397-A 1 13-DEC-1995;
BOEHRINGER MANNHEIM GMBH (DE)
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US-09-944-884-2 (1-379) x AB037269 (1-2960)

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Qy 273 snAsnLysIleThrAspIleGluAsnGlySerLeuAlaAsnIleProArgValArgGluI 293
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Qy 313 euGlnIleIlePheLeuHisSerAsnSerIleAlaArgValGlyValAsnAspPheCysP 333
Db 1170 TGCAGTGTGTATCTGCATCTCAACAACATCACCAGGTGGCGTCAATGACTTCTGCC 1229
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Qy 373 lnLeuGlyAsnPhe 377
Db 1350 AGTTTGGCAATTAC 1363

RESULT 13
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DEFINITION Sequence 1 from Patent EP0686397.
ACCESSION A77048
VERSION A77048.1 GI:6088837
KEYWORDS
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Koops, A. and Hasenoehl, R.D.
TITLE USE OF CHONDROITIN SULPHATE PROTEOGLYCAN FOR PROTECTION OF NEURONS
JOURNAL Patent: EP 0686397-A 1 13-DEC-1995;
BOEHRINGER MANNHEIM GMBH (DE)
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BASE COUNT 859 a 667 c 652 g 782 t
ORIGIN

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[illegible]





GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus.p2n model

Run on: May 31, 2003, 13:44:02 : Search time 1779 Seconds  
(without alignments)  
3450.303 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1992

Sequence: 1 MREYVLLLELALCSAKPFPS.....PATRCVLSRMSVOLGNFGM 379

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pcpt -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=score -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09944884 -CGN\_1\_1\_1906 -runat\_27052003\_150250\_7733 -NCPU=6 -ICPU=3  
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Database :

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6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: gb\_gss:\*  
18: em\_gss\_hum:\*  
19: em\_gss\_inv:\*  
20: em\_gss\_pln:\*  
21: em\_gss\_vrt:\*  
22: em\_gss\_fun:\*  
23: em\_gss\_man:\*  
24: em\_gss\_mus:\*  
25: em\_gss\_other:\*  
26: em\_gss\_pro:\*  
27: em\_gss\_rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1790	89.9	2302	11	AK014504	AK014504 Mus muscu
2	1112	55.8	926	14	BQ960688	BQ960688 AGENCOURT
3	1035.5	52.0	695	10	AM608047	AM608047 RC3-LT002
4	978	49.1	553	9	AL598934	AL598934 DKEZ313F
5	922.5	46.3	1159	12	BF164270	BF164270 601773027
6	912	45.8	641	10	BE374603	BE374603 601225391
7	911	45.7	568	9	AI006670	AI006670 ue16b10.Y
8	893	44.8	936	14	BQ882271	BQ882271 AGENCOURT
9	845	42.4	592	9	AL600795	AL600795 DKEZP313E
10	822	41.3	839	14	BQ942694	BQ942694 AGENCOURT
11	818	41.1	865	9	AI789337	AI789337 UK53H09.Y
C 12	808.5	40.6	995	9	AL568847	AL568847 AL568847
C 13	804.5	40.4	879	9	AL571404	AL571404 AL571404
14	797	40.0	974	9	AL541759	AL541759 AL541759
15	777	39.0	955	14	BQ708510	BQ708510 AGENCOURT
C 16	760.5	38.2	824	9	AL571461	AL571461 AL571461
C 17	732.5	36.8	956	9	AL541055	AL541055 AL541055
18	727	36.5	996	12	BG111541	BG111541 602282864
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20	720	36.1	943	14	BQ900541	BQ900541 AGENCOURT
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26	698.5	35.1	943	14	BQ941521	BQ941521 AGENCOURT
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28	692.5	34.8	1039	9	AL540886	AL540886 AL540886
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30	686.5	34.5	957	9	AL540527	AL540527 AL540527
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# ALIGNMENTS

RESULT 1

AK014504

LOCUS

DEFINITION

AK014504

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AK014504 2302 bp mRNA linear HTC 19-JAN-2002  
Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched  
library, clone:4631401G09:asporin, full insert sequence.

AK014504.1 GI:12852406

HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA,

clone.lib:RIKEN full-length enriched mouse cDNA library

clone:4631401G09.

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

## AUTHORS

**AUTHORS** Carninci, P. and Hayashizaki, Y.  
**TITLE** High-efficiency full-length cDNA cloning  
**JOURNAL** Meth. Enzymol. 303, 19-44 (1999)  
**MEDLINE** 99279253  
**PUBMED** 10349636

## REFERENCE

2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. <i>Genome Res.</i> 10 (10), 1617-1630 (2000).
JOURNAL	20499374
MEDLINE	11042159
PUBLISHED	

## REFERENCE

3 Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
Riken integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
JOURNAL MEDLINE  
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## REFERENCE

4 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamanka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kusakawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaïdo, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carinci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustinch, S., Hill, D., Hofmann, M., Hume, D. A., Kaniya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, H., Kohtsuki, S.

and Hayashizaki, Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6821), 685-690 (2001)  
21085860  
MEDLINE  
PUBMED  
11217851  
5 (bases 1 to 2302)  
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,  
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Hayashizaki, Y.

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ACCESSION BQ960688
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SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 926)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: Susan L. Sullivan, Ph.D.
cDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLML at:
http://image.llnl.gov
Plate: LUAMI3741 row: g column: 13
High quality sequence stop: 710.
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BASE COUNT 287 a 194 c 171 g 272 t 2 others
ORIGIN
Alignment Scores:
Pred. No.: 1.37e-122 Length: 926
Score: 1112.00 Matches: 219
Percent Similarity: 92.37% Conservative: 11
Best Local Similarity: 87.95% Mismatches: 13
Query Match: 55.82% Indels: 8
DB: 14 Gaps: 1
US-09-944-884-2 (1-379) x BQ960688 (1-926)
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Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
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Db 718 ACATTCCACCGCGTGCACCTTGCAGATCTCAACCGGTTCAGGACCTCGGCACAGGTG 777
Qy 270 lyLeuGlyAsnAsnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 290
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Qy 290 alArgGluLleHisLeuGluAsnAsnLysLeu----- 300
Db 819 -----CACAGGACAGAAACCAAGCTCTCAACACATCATCAGGACACCCACACACA 867
Qy 301 --LysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 314
Db 868 ACCAACCAACCACTCGGATGCGGAGGAGTCAACACACCCCAAGAAACA----- 917
Qy 314 lnllelPheLeuHisSerAsnSerlleAlaArgValGlyValAsnAspPheCysPro 334
Db 918 -----TGCCACAGCACAAACCGCACCGCCACAGCGGCATCACACTACACTCGCG 966
Qy 334 hrValPro 336
Db 967 ACGGCCCG 974

RESULT 6
BE374603
LOCUS 601225391F1 NCI_CGAP_Mam1 Mus musculus cdna linear EST 21-JUL-2000
DEFINITION mRNA sequence.
ACCESSION BE374603
VERSION BE374603.1 GI:9319966
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryote; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 641)
REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapb-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
```

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cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LAM8740 row: f column: 23
High quality sequence stop: 602.
Location/Qualifiers
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/strain="FVB/N"
/db_xref="taxon:10090"
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
BASE COUNT 230 a 117 c 131 g 162 t 1 others
ORIGIN
Alignment Scores:
Pred. No.: 8,18e-99 Length: 641
Score: 912.00 Matches: 189
Percent Similarity: 94.37% Conservative: 12
Best Local Similarity: 88.73% Mismatches: 10
Query Match: 45.78% Indels: 5
DB: 10 Gaps: 1
US-09-944-884-2 (1-379) x BE374603 (1-641)
Qy 162 SerGluLleProLeuAsnLeuProLysSerLeuAlaGluLeuArgLleHisLysLys 181
Db 2 ACTGAATTCACCTTAATCTTCCCAATCACTTAGCAGAACTCAGAAATTCATGATAATAA 61
Qy 182 ValLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 201
Db 62 GTTAAGAAGATACAAAAGGACACAGCTTCAAGGGAATGAATGCTTTACATGTTTGAATG 121
Qy 202 SerAlaAsnProLeuAsnAsnGlyLleGluProGlyAlaPheGluGlyValThrVal 221
Db 122 AGTCAAAACCTCTTGAGAACACAGGAGTAGAACAGGGGCACTTTGAAGGGGTGACAGTA 181
Qy 222 PheHisLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 241
Db 182 TTCATATCAGATCGCTGGAAGCAAACTACCTCAATTCACAAAGGCTTACCACCAACT 241
Qy 242 LeuLeuGluLeuHisLeuAspTyrAsnLysLysLysLysLysLysLysLysLysLys 261
Db 242 TTGCTGGAGCTTCATTTAGATTTTAAATAAATTTCAACGGTGAAGATCTTAA 301
Qy 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysLysLysLysLysLys 281
Db 302 CGGTACAGGGAACCTCAAAAGCTGGTCTTGAACAAACAGAAATCACAGATATTTGAAAT 361
Qy 282 GlySerLeuAlaAsnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 301
Db 362 GGAACCTT-GCTAATATATACACGCTGTGAGAGAGATACACTTGGAAACAAATAAATAA 420
Qy 302 LysLysProSerGlyLeuProGluLeuLysLysLysLysLysLysLysLysLysLys 321
Db 421 AAATCCCTTCAGGATTCAGAGAGTGAATAACCTCCAGATAATCTCTTCATATAAT 480
Qy 322 SerLleAlaArgValGlyValAsnAspPheCysProThr-ValProLysMetLysLysSe 341
Db 481 TCAATGTCAAAGTGGGAGTGAATGACTTCTGTCCACAGAGTCCAAAGATGAAGAAATC 540
Qy 341 rLeuTyrSerAlaLysLeuPheAsnProValLysTyrTrpGluMetGlnProAl 361
Db 361
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cdna Library Preparation: Life Technologies, Inc.  
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LAM8740 row: f column: 23  
High quality sequence stop: 602.  
Location/Qualifiers  
1..641  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone="IMAGE:3583510"  
/clone\_lib="NCI\_CGAP\_Mam1"  
/tissue\_type="tumor, biopsy sample"  
/dev\_stage="10 months, virgin"  
/lab\_host="DH10B"  
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: SalI;  
Site:2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

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Db      541 TTTATACGTGCAATAAGTTTATTCAACCAACCAATGAAGTACTGGGAATACA-CCTGC 599
QY      361 aThrPheArgCysValLeuSerArgMetSerValGln 373
Db      600 A---CAATGCTGTGTTCTGG--CGAATGAGTGTCAG 631

RESULT 7
AI006670
LOCUS   568 bp mRNA linear EST 12-JUN-1998
DEFINITION uel6b10.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
IMAGE:1480507 5' similar to SW:PGSI_HUMAN P21810 BONE/CARTILAGE
PROTEOLYCAN I PRECURSOR ;, mRNA sequence.
ACCESSION AI006670
VERSION   1
KEYWORDS  house mouse;
SOURCE    Mus musculus
ORGANISM  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
REFERENCE 1 (bases 1 to 568)
AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
          Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
          Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
          Theising,B., Wylie,T., Lennon,G., Soares,B., Willson,R. and
          Waterston,R.
TITLE     The WashU-HMI-Mouse EST Project
JOURNAL   Unpublished (1996)
COMMENT   Contact: Marra M/Mouse EST Project
          WashU-HMI Mouse EST Project
          Washington University School of MedicineP
          4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
          Tel: 314 286 1800
          Fax: 314 286 1810
          Email: mouseest@watson.wustl.edu
          This clone is available royalty-free through LLNL ; contact the
          IMAGE Consortium (info@image.llnl.gov) for further information.
          MGI:928863
          Possible reversed clone: similarity on wrong strand
          Seq primer: primer name ambiguous
          High quality sequence stop: 371.

FEATURES
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            /strain="C57BL"
            /db_xref="taxon:10090"
            /clone="IMAGE:1480507"
            /dev_stage="embryo, 14 dpc"
            /lab_host="DH10B"
            /notes="Vector: pME18S-FL3; Site 1: DraIII (CACTGTGTG);
            Site 2: DraIII (CACCATCTG); 1st strand cDNA was primed
            with an oligo(dT) primer [ATGTGCCCTTTTCTTTTCTTTT];
            double-stranded cDNA was ligated to a DraIII adaptor
            [TGTGGCTACTGG], digested and cloned into distinct DraIII
            sites of the pME18S-FL3 vector (5' site CACTGTGTG, 3' site
            CACCATCTG). XhoI should be used to isolate the cDNA
            insert. Size selection was performed to exclude fragments
            <1.5kb. Library constructed by Dr. Sumio Sugano
            (University of Tokyo Institute of Medical Science).
            Custom primers for sequencing: 5' end primer
            CTCTGCTCTAAAGCTGCG and 3' end primer
            CGACCTGCGACTCGACACA."
BASE COUNT 193 a 124 c 94 g 157 t
ORIGIN

Alignment Scores:
Pred. No.:      8.91e-99      Length:      568
Score:          911.00      Matches:      172
Percent Similarity: 91.79%      Conservative: 7
Best Local Similarity: 88.21%      Mismatches: 10
Query Match:      45.73%      Indels:      6
DB:              9          Gaps:      1

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US-09-944-884-2 (1-379) x AI006670 (1-568)
QY      11 AlaLeuCysSerAlaLysProPheSerHisIleAlaLeuLysAsnMetMet 30
Db      2 GCTGTGCTCTGCCAAACCTTCTTTAGCCCTTCCACACAGCACTGAAGATATGATG 61
QY      31 LeuLysAspMetGluAspThrAspAspAspAspAspAspAspAspAspAsp 50
Db      62 TTGAAGGATATGAAGACACAGATGATGACGATAAGCATGATGAC----- 106
QY      51 GluAspAsnSerLeuPheProThrArgGluProArgSerHisPhePheProPheAspLeu 70
Db      107 ---GACAACCTCTCTTTTCCACGAAGAGCAGTAGTGAACCCCTTTTCCCTTCGATTG 163
QY      71 PheProMetCysProPheGlyCysGlnCysTyrSerArgValValHisCysSerAspLeu 90
Db      164 TTTCACCATGTCCTATTTGGTGCCCAATGTACTCTCGAGTCTTCACTGCTGATCTA 223
QY      91 GlyLeuThrSerValProThrAsnIleProPheAspThrArgMetLeuAspLeuGlnAsn 110
Db      224 GGCTGACATCGGTTCACAAACACATTCCTATTTGATCTCGAATGGTTGACCTTCAAAAT 283
QY      111 AsnLysIleLysGluIleLysGluAsnAspPheLysGlyLeuThrSerLeuTyrGlyLeu 130
Db      284 AATAAATCAAGGAATTAAGAAATGACTTTAAGGACTCACTTCACCTTATGCTCTG 343
QY      131 IleLeuAsnAsnLysLeuThrLysIleHisProLysAlaPheLeuThrThrLysLys 150
Db      344 ATTCTGAACAACAACAGCTAACAAAGATTCAACCAAAACCTTCTTACCAACAACAA 403
QY      151 LeuArgGluLeuTyrLeuSerHisAsnGlnLeuSerGluIleProLeuAsnLeuProLys 170
Db      404 TTGAGAAGGCTATATTATCCCAACCACTAAGTGAATTCACCTTAATCTTCCAGA 463
QY      171 SerLeuAlaGluLeuArgIleHisGluAsnLysValLysLysIleGlnLysAspThrPhe 190
Db      464 TCATTAGCAGACTCAGAAATCATGATAATAAAGTAAGAGATTCAAAAGGACACGTT 523
QY      191 LysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnPro 205
Db      524 AAGGGAATGAATGCTTTTACATGTTTGGAAATGAGTTGCAAAACCC 568

RESULT 8
BQ882271
LOCUS    936 bp mRNA linear EST 16-AUG-2002
DEFINITION AGENCOURT 7982177 Lupski_dorsal_root_ganglion Homo sapiens CDNA
clone IMAGE:6186197 5', mRNA sequence.
ACCESSION BQ882271
VERSION   BQ882271.1
KEYWORDS  EST.
SOURCE    human.
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 936)
AUTHORS   NTH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cygabs-remail.nih.gov
          Tissue Procurement: Dr. James R. Lupski
          cDNA Library Preparation: Life Technologies, Inc.
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: LLAM13578 row: d column: 06
          High quality sequence stop: 637.
          Location/Qualifiers
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              /organism="Homo sapiens"
              /db_xref="taxon:9606"

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/clone="IMAGE:6186197"
/clone.lib="Lupski_dorsal_root_ganglion"
/sex="male"
/tissue.type="dorsal_root_ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
Note: pcMV-SPORT6 (Life Technologies); Site_1:
Not1; Site_2: Salt; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCTGCTAGCTGAGCGGCGGCGCT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies.

```

BASE COUNT 222 a 309 c 246 g 158 t 1 others

Alignment Scores:  
 Pred. No.: 2,85e-96 Length: 936  
 Score: 893.00 Matches: 164  
 Percent Similarity: 77.66% Conservatives: 55  
 Local Similarity: 58.16% Mismatches: 62  
 Query Match: 44.83% Indels: 1  
 DB: 14 Gaps: 0

US-09-944-884-2 (1-379) x B0882271 (1-936)

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QY 95 ValProThrAsnIleProPheAspThrArgMetLeuAspLeuGlnAsnLysIleLys 114
DB 2 GTGCCAAGAGATCTCCCTGCACACCGCTGCTGGAGCTGCAGAACACGACATCTCC 61

QY 115 GluIleLysGluAsnAspPheLysGlyLeuThrSerLeuTyrglyLeuIleLeuAsnAsn 134
DB 62 GAGCTCCGCAAGGATGACTCAAGGCTCTCCAGCACCTTACGCCCTCGCTGCTGTAAC 121

QY 135 AsnLysLeuThrLysIleHisProLysAlaPheLeuThrLysLysLysArgArgLeu 154
DB 122 AACAGATCTCCAAAGTCCATGAGAAGGCTTACGCCACCTGCGGAGAGTGTTCAGCGGCTCCGG 301

QY 155 TyrLeuSerHisAsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGlu 174
DB 182 TACATCTCCAGAACACCTGCTGGAGATCCCGCCCACTTACCCAGCTCTCCCTGGTGAG 241

QY 175 LeuArgIleHisGluAsnLysValLysIleGlnLysAspThrPheLysGlyMetAsn 194
DB 242 CTCGCGATCCAGCAACCGCATCCGCAAGGTGCGCAAGGAGTGTTCAGCGGCTCCGG 301

QY 195 AlaLeuHisValLeuGluMetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGly 214
DB 302 AACATGAACCTGATCGAGATGGCGGGAACCCACTGGAGAACAGTGGCTTTGAACCTGGA 361

QY 215 AlaPheGluGlyValThrValPheHisIleArgIleAlaGluAlaLysLeuThrSerVal 234
DB 362 GCCTTCGATGGCTGAAGCTCACTACCTGCGCATCTCAGAGCCCAAGCTGACTGGCATC 421

QY 235 ProLysGlyLeuProProThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThr 254
DB 422 CCCAAAGACCTCCCTGAGACCTGTAATGAATCCACCTAGACCACACAAATCCAGGCC 481

QY 255 ValGluLeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsn 274
DB 482 ATCGAAGCTGGAGGAGCTGCTGCTGCTACTCCAAAGCTGTACAGGCTGGGCTGAGGCCAAC 541

QY 275 LysIleThrAspIleGluAsnGlySerLeuAlaAsnIleProArgValArgGluIleHis 294
DB 542 CAGATCAGATGATCGAAGACGGAGGAGCTGAGCTCTCCACCTCCGGGAGCTCCAC 601

QY 295 LeuGluAsnAsnLysLysIleProSerGlyLeuProGluLeuLysTyrLeuGln 314
DB 602 TTGGACAACAACAACTTGCCCGAGGCTGCCCTCAGGGCTCCAGACCTCAAGCTCCTCCAG 661

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QY 315 IleIlePheLeuHisSerAsnSerIleAlaArgValGlyValAsnAspPheCysProThr 334
DB 662 GTGGTCTATCTGCACCTCCAAACATCACCAGAGGGGTGTACAGACTTCTGTCCCATG 721

QY 335 ValProLysMetLysSerLeuTyrglySerAlaIleSerLeuPheAsnProVal-Ly 354
DB 722 GCGTTCGGGTGAAGCGGGCTTACTACACGGCATCAGCCTCTTCAACACCGCGTGCC 781

QY 354 sTyTrpGluMetGlnProAlaThrPheArgCysValLeuSerArgMetSerValGlnLe 374
DB 782 CTACTGGGAGTGCAGCGGCGCTTCCGCTGCTGCTACTACCGCGCTGGNCATCCAGTT 841

QY 374 uGly 375
DB 842 TGGG 845

RESULT 9
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LOCUS DKEZp313E0538_r1 313 (synonym: hlcc2) Homo sapiens cDNA clone
DEFINITION DKEZp313E0538 5', mRNA sequence.
ACCESSION AL600795
VERSION AL600795.1 GI:15164301
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Wambutt,R., Heubner,D., Mewes,W., Weil,B. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B. and Wiemann,S.)
JOURNAL Unpublished (1999)
COMMENT Contact: Wambutt R
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFZp313E0538) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
FEATURES
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1..592
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/db_xref="taxon:9606"
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/note="Vector: pTriplex2; Site_1: Sf1A; Site_2: Sf1B;
cDNA-collection"
BASE COUNT 180 a 124 c 110 g 178 t
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Pred. No.: 8.09e-91 Length: 592
Score: 845.00 Matches: 157
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 42.42% Indels: 0
DB: 9 Gaps: 0
US-09-944-884-2 (1-379) x AL600795 (1-592)
QY 1 MetLysGluTyrValLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
DB 121 ATGAGGAGTAGTGTCTCTCTATTATCTGCTGTGCTGCTGCAACCCCTCTTTAGC 180
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
DB 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40

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Db      181 CCTTCACACATCCGACTGAAGAATATATGCTCAAGGATATGAAGACACACAGATGATGAT 240
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Db      241 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
QY      61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db      301 CCAAGAGGCCAATTTTTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
QY      81 TyrSerArgValHisCysSerAspLeuGlyLeuThrSerValProThrAsnLeuPro 100
Db      361 TATTCACGAGTGTACATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCAT
QY      101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysLysLysLysLysLysLysLysLysLys
Db      421 TTGTATCTCGAATGCTGATCTTCAACAAATATTAATTAATTAATTAATTAATTAATTAATTA
121 PheLysGlyLeuThrSerLeuThrGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu
Db      481 TTTAAAGGACTCATTCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT
QY      141 HisProLysAlaPheLeuThrLysLysLysLysLysLysLysLysLysLysLysLysLysLys
Db      541 CACCCCAAAAGCCCTTCTAACCACAAAGAGTTGCCGAAGGCTGTATCTGTCC 591

RESULT 10
BQ942694
LOCUS
DEFINITION
IMAGE:6205396 5', mRNA sequence.
ACCESSION
BQ942694
VERSION
BQ942694.1 GI:22358172
KEYWORDS
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 839)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaops-remail.nih.gov
Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLMI3628 row: d column: 05
High quality sequence stop: 605.
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/dev_stage="adult, 70 yr"
/lab_host="DH10B"
./note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
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5'-GACTAGTCTTAGTCGCGGCGGCGGCTT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

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## FEATURES

source

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BASE COUNT 198 a 280 c 213 g 147 t 1 others
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Alignment Scores:
Score: 8.14e-88 Length: 839
Pred. No.: 822.00 Matches: 157
Percent Similarity: 78.11% Conservatives: 50
Best Local Similarity: 59.25% Mismatches: 54
Query Match: 41.27% Indels: 4
DB: 14 Gaps: 0
US-09-944-884-2 (1-379) x BQ942694 (1-839)
QY 73 MetCysProPheGlyCysGlnCysTyrSerArgValHisCysSerAspLeuGlyLeu 92
Db 4 ATGTGCTCTTTCGGTGGCTGCCACTGCCACCTGCGGTGGTTCAGTGTCCAGACCTGGCTGTG 63
QY 93 ThrSerValProThrAsnLeuProPheAspThrArgMetLeuAspLeuGlnAsnLys 112
Db 64 AAGTCTGTGCTGCCCAAGAGATCTCCCTGACACACACGCTGCTGGACCTGCAGAACACGAC 123
QY 113 IleLysGluIleLysGluAsnAspPheLysGlyLeuThrSerLeuThrGlyLeuLeu 132
Db 124 ATCTCGAGCTCGGCAAGGATGACTTCAAGGTCTCCAGCACCTCTACGCCCTCGTCTG 183
QY 133 AsnAsnAsnLysLeuThrLysLysLysLysLysLysLysLysLysLysLysLysLysLys 152
Db 184 GTGAACAACAAGATCTCCAAGATCCATGAGAAGGCTTCAGCCACCTGCGGAAGCTGCAG 243
QY 153 ArgLeuThrLysSerHisAsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeu 172
Db 244 AAGCTCTACATCTCCAAGAACACCACTGGTGGAGATCCCGCCCACTACCCAGCTCCCTG 303
QY 173 AlaGluLeuArgIleHisGluAsnLysValLysLysLysLysLysLysLysLysLysLys 192
Db 304 GTGGAGCTCCGATCCACGACACACACACACACACACACACACACACACACACACACAC 363
QY 193 MetAsnAlaLeuHisValLeuGluMetSerAlaAsnProLeuAspAsnAsnGlyIleGlu 212
Db 364 CTCGGCAACATGAATCGATCGATGAGTGGCGGGAACCCACTGGAGAACAGTGGCTTTGA 423
QY 213 ProGlyAlaPheGluGlyValThrValPheHisIleArgIleAlaGluAlaLysLeuThr 232
Db 424 CTTGGAGCCTTCGATGGCTGGAAGCTCAACTCGCTGCACTTCAGAGGCCAAGCTGACT 483
QY 233 SerValProLysGlyLeuProThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLys 252
Db 484 GGCATCCCAAGACACCTCCCTGAGACCTGGAATGAACTCCACCTAGACACACACAAATC 543
QY 253 SerThrValGluLeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuGly 272
Db 544 CAGGCCATCGAATCGGAGGACCTGCTTCGCTACTCCAAAGCTGTACAGGCTGGCGCTAGGC 603
QY 273 AsnAsnLysIleThrAspIleGluAsnGlySerLeuAlaAsnLeuProArgValArgGlu 292
Db 604 CACAACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
QY 293 IleHisLeuGluAsnAsnLysLysLysLysLysLysLysLysLysLysLysLysLysLys 312
Db 664 CTCACCTGGACCAACAAGTTGGCCAGGCTGCTCCAGGCTCCAGGCTCCAGGCTCCAGGCT 723
QY 312 rLeuGln-IleIlePheLeuHisSerAsnSerIleAla-ArgValGlyValAsnAsp-Ph 331
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LOCUS
DEFINITION
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 /lab\_host="PH10B"  
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 cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-stranded cDNA was digested with Not I  
 and cloned into the Not I and Eco RV sites of the  
 pCMVSPORT 6 vector. Library was constructed by Life  
 Technologies, Contact : Feng Liang Life Technologies, a  
 division of Invitrogen 9800 Medical Center Drive Rockville  
 , Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
 fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"

BASE COUNT 255 a 195 c 222 g 315 t 8 others  
 ORIGIN

Alignment Scores:  
 e: 4.46e-86 Length: 995  
 e: 808.50 Matches: 149  
 Percent Similarity: 75.28% Conservative: 55  
 Best Local Similarity: 54.98% Mismatches: 66  
 Query Match: 40.59% Indels: 1  
 DB: 9 Gaps: 1

US-09-944-884-2 (1-379) x AL568847 (1-995)

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 QY 128 TyrGlyLeuLeuAsnAsnLysLeuThrLysLysLysProLysAlaPheLeuThr 147  
 DB 934 CAGCGATTGATCTTTCACACATAAATAGCAAGATTAGTCTCGAGGATTACACCT 875  
 QY 148 ThrLysLysLeuArgLysLeuSerHisAsnGlnLeuSerGluLeuProLeuAsn 167  
 DB 874 TTGGTGAAGTTGACGACTTTATCTGTCCAGAAATCAGCTGAAGAAATGCCAGAAAA 815  
 QY 168 LeuProLysSerLeuAlaGluLeuArgLysGluAsnLysValLysLysLysGlnLys 187  
 DB 814 ATCCCAAACTCTTCAGAGCTGCGTGCCCATGAGTATGAGTACCAAGAGTCCGAAAA 755  
 QY 188 AspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnProLeuAsp 207  
 DB 754 GTTACTTTCAATGAGTACGACCATGATGTTGCATAGAACTGGCGACCAATCCGCTGAAG 695  
 QY 208 AsnAsnGlyLeuProGlyAlaPheGluGlyVal---ThrValPheHisLysLeuArgLys 226  
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 QY 227 AlaGluAlaLysLeuThrSerValProLysGlyLeuProProThrLeuLeuGluHis 246  
 DB 634 GGTGATACCAATATCCAGCATCTCTGCTGTTTGCACAAATGCTCTCTGGCCCAAC 575  
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 QY 267 GlnArgLeuGlyLeuGlyAsnAsnLysLysLeuAspLysGluAsnGlySerLeuAlaAsn 286  
 DB 514 GCTAAGTTGGATTGATTTCAACAGCATCTCTGCTGTTTGCACAAATGCTCTCTGGCCCAAC 455  
 QY 287 IleProArgValArgLysLysLeuGluAsnAsnLysLysLysLysLysLysProSerGly 306  
 DB 454 ACGCCTCATCTGAGGAGCTTCACTTGGACAAACAAGCTTACCAGAGTACCTGGTGGG 395  
 QY 307 LeuProGluLeuLysTyrLeuGlnLysLysLysLysLysLysLysLysLysLysLysLys 326  
 DB 394 CTGGCAGAGCATAGTATCATCAGGTTGCTACCTTCATACCAATATCTCTGTAGTT 335  
 QY 327 GlyValAsnAspPheCysProThrValProLysMetLysLysLysLysLysLysLysLys 346  
 DB 334 GGATCAAGTCACTCTGCCCACCTCCGACACACACCAACCAAGGCTCTTATTTCGGGTGTG 275

QY 347 SerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAlaThrPheArgCysVal 366  
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 QY 367 LeuSerArgMetSerValGlnLeuGlyAsnPhe 377  
 DB 214 TACGTGGCTCTGCCATTCATCACTCGGAAACTAT 182  
 RESULT 13  
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 DEFINITION AL571404 LTI\_NFL006\_PL2 Homo sapiens cDNA clone CSODI023YG19 3  
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 ACCESSION AL571404  
 VERSION AL571404.1 GI:12928667  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 879)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 Evry cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
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 was primed with a NotI-oligo(dT) primer. Five prime end  
 enriched, double-stranded cDNA was digested with Not I and  
 cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
 vector. Library was normalized. Library was constructed by  
 Life Technologies, Contact : Feng Liang Life Technologies,  
 a division of Invitrogen 9800 Medical Center Drive  
 Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"

BASE COUNT 223 a 179 c 204 g 270 t 3 others  
 ORIGIN

Alignment Scores:  
 Pred. No.: 1.11e-85 Length: 879  
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 Percent Similarity: 75.00% Conservative: 55  
 Best Local Similarity: 54.78% Mismatches: 67  
 Query Match: 40.39% Indels: 1  
 DB: 9 Gaps: 1

US-09-944-884-2 (1-379) x AL571404 (1-879)

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 QY 127 LeuTyrGlyLeuLeuAsnAsnLysLysLysLysLysLysLysLysLysLysLysLys 146  
 DB 817 CTTCAAGCATTTGTTCTTGTCAACAATAAATAGCAAAAGTTAGTCTCGGAGCATTTACA 758  
 QY 147 ThrThrLysLysLeuArgLysLeuSerHisAsnGlnLeuSerGluLeuProLeu 166  
 DB 757 CCTTTGTGTAAGTTGGAACGACTTTATCTTCAAGAAATCAGCTGAAGGAATTCAGCA 698  
 QY 167 AsnLeuProLysSerLeuAlaGluLeuArgLysLysLysLysLysLysLysLysLys 186  
 DB 697 AAATGCCAAACTCTTCAGGAGCTCGTCCCATGAGATGAGATGATGATGATGATGATG 638

187 LysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMetSerAlaAsnProLeu 206  
 637 AAAGTTACTTTCAATGGACTGAACACAGATGTTGTATAGAACTGGGACCAATCCGCTG 578  
 207 AspAsnGlyLeuGluProGlyAlaPheGluGlyVal---ThrValPheHisIleArg 225  
 577 AAGAGCTCAGGAATGAAATGGGGCTTCCAGGGAATGAAGAAGCTCTCTACATCCGC 518  
 226 IleAlaGluAlaLysLeuThrSerValProLysGlyLeuProProThrLeuLeuGluLeu 245  
 517 ATTGCTGATACCAATATACACAGCATCTCTCAAGGTCTCTCTCTCTCTCTCTCTCT 458  
 246 HisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLysArgTyrLysGlu 265  
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 286 AsnIleProArgValArgGluLeuHisLeuGluAsnLysLeuLysIleProSer 305  
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 326 ValGlyValAsnAspPheCysProThrValProLysMetLysLysSerLeuTyrSerAla 345  
 217 GTTGGATCAAGTKAYTTCTGCCACCTGGACACACACCAAAAGGCTTCTTATTCGGGT 158  
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 157 GTGAGTCTTTTCAGCAACCGGTCCAGTACTGGAGATACAGCCATCCACCTTCAGATG 98  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 974)  
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 Location/Qualifiers  
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 cDNA was primed with a NotI-oligo(dT) primer. Five prime  
 end enriched, double-stranded cDNA was digested with Not I  
 and cloned into the Not I and Eco RV sites of the  
 pCMVSPORT 6 vector. Library was constructed by Life

Technologies. Contact : Feng Liang Life Technologies, a  
 division of Invitrogen 9800 Medical Center Drive Rockville  
 Maryland 20850, USA Fax : (1) 301 610 8371 Email :  
 fliang@lifetech.com URL :  
 http://fulllength.invitrogen.com"

BASE COUNT 284 a 231 c 203 g 248 t 8 others  
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Alignment Scores: 1.04e-84 Length: 974  
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 Score: 72.79% Conservative: 55  
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 Query Match: 9 Gaps: 2  
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US-09-944-884-2 (1-379) x AL541759 (1-974)

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 Db 61 AAAGTGCCTAAGATCTTCCCTCTGACACAACTCTGCTAGACCTGCAACACAAATA 120  
 Qy 114 LysGluIleLeuGluAsnAspPheLysGlyLeuThrSerLeuTyrGlyLeuLeuAsn 133  
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 Qy 194 AsnAlaLeuHisValLeuGluMetSerAlaAsnProLeuAspAsnGlyIleGluPro 213  
 Db 361 AACAGATGATTGTATAGAACTGGGACCAATCCCTGAGAGCTCAGAAATGAAAT 420  
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 Qy 273 AsnAsnLysIleThrAspIleGluAsnGlySerLeuAlaAsnIleProArgValArgGlu 292  
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 Qy 333 ProThrValProLysMetLysLysSerLeuTyrSerAlaIleSerLeuPheAsnPro 352  
 Db 780 CCACCTGGACACACACCAAAAGGCTTCTTATTCGGGTGTGAGT---YTTTCAGCAGCCC 836

Qy	353	vallystryrtrpGlumetGlnProAlaThrPheargCysVal 366
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ACCESSION	BQ708510	
VERSION	BQ708510.1	GI:21847409
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ORGANISM	Homo sapiens	
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	1 (bases 1 to 955)	
	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	
	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	
	Contact: Robert Strausberg, Ph.D.	
	Email: cgapbs-re@mail.nih.gov	
	Tissue Procurement: Dr. Mark Watson	
	cDNA Library Preparation: Rubin Laboratory	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
	DNA Sequencing by: Agencourt Bioscience Corporation	
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	
	Plate: L12CM382 row: c column: 22	
	High quality sequence start: 6	
	High quality sequence stop: 663.	
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ORIGIN		
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Qy	163	GluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsnLysVal 182
Db	63	GAGATCCGCGCCCACTACCCAGCTCCCTGGTGGAGCTCCGCATCCAGACAACCGCATC 122
Qy	183	LysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMetSer 202
Db	123	CGAAGTGCCCAAGGAGGTGTTCCAGCGGGCTCCGGAACTGAATCTGCATCGATGGCC 182



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: May 31, 2003, 10:29:02 ; Search time 6337 Seconds  
(without alignments)  
11270.047 Million cell updates/sec

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Perfect score: 2454  
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Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb.om : \*  
5: gb.ov : \*  
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8: gb.pl : \*  
9: gb.pr : \*  
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26: em.ro : \*  
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28: em.un : \*  
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41: em.htgo\_other : \*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2454	100.0	2454	6	AX454444	AX454444 Sequence
3	2454	100.0	2454	6	AX464194	AX464194 Sequence
4	2454	100.0	2454	6	AX490922	AX490922 Sequence
5	2403.8	98.0	2466	9	AY029191	AY029191 Homo sapi
6	1862.8	75.9	1903	9	AK000136	AK000136 Homo sapi
7	1786.8	72.8	2089	9	AK027359	AK027359 Homo sapi
8	1254.8	51.1	152341	9	AL137848	AL137848 Human DNA
9	1184	48.2	1184	9	AF316824	AF316824 Homo sapi
10	1122.6	45.7	2325	10	BC034888	BC034888 Mus muscu
11	911	37.1	1165	10	AF316825	AF316825 Mus muscu
12	462	18.8	496	6	AX210520	AX210520 Sequence
13	368	15.0	1634	5	AF247821	AF247821 Oreochrom
14	367.8	15.0	2960	5	AB037269	AB037269 Xenopus l
15	328.8	13.4	263505	2	AC123954	AC123954 Mus muscu
16	312	12.7	2446	10	RN017834	U17834 Rattus norv
17	310.4	12.6	1107	6	A77048	A77048 Sequence 1
18	305.8	12.5	182798	2	AC025394	AC025394 Homo sapi
19	305.2	12.4	1492	4	AF125537	AF125537 Sus scrof
20	303.2	12.4	2072	5	AF247822	AF247822 Oreochrom
21	301	12.3	964	4	OC003394	U03394 Oryctolagus
22	301	12.3	1553	4	S76584	S76584 decorin-pro
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28	296.2	12.1	1311	10	RNDCNMR	Z12298 R.rattus mR
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31	295.4	12.0	1026	6	AF012319	AF012319 Sequence
32	295.4	12.0	1026	6	I27828	I27828 Sequence 1
33	295.4	12.0	1080	9	AF138300	AF138300 Homo sapi
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36	295.4	12.0	1837	6	AX014351	AX014351 Sequence
37	294.6	12.0	1685	6	AX146889	AX146889 Sequence
38	294.6	12.0	1685	6	AX148653	AX148653 Sequence
39	294.6	12.0	1685	6	AX330891	AX330891 Sequence
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VERSION  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL

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human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
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Baker,K.P., Chen,J., Goddard,A., Gurney,A.L., Wood,W.I. and Yuan,J.  
Polypeptides and nucleic acids encoding the same  
Patent: EP 1191101-A 1 27-MAR-2002;  
linear PAT 05-JUN-2002





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LOCUS AX464194 2454 bp DNA linear PAT 16-JUL-2002  
DEFINITION Sequence 327 from Patent WO0140466.  
ACCESSION AX464194  
VERSION AX464194.1 GI:21899113  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS Baker,K.P., Beresini,M., Deforge,L., Desnoyers,L., Filvaroff,E.,  
Gao,W.Q., Gerritsen,M.E., Goddard,A., Godowski,P.J., Gurney,A.L.,  
Sherwood,S., Smith,V., Stewart,T.A., Tumas,D., Watanabe,C.K.,  
Wood,W.L. and Zhang,Z.  
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding  
same  
JOURNAL Patent: WO 0140466-A 327 07-JUN-2001;  
Genentech Inc. (US)  
FEATURES  
Location/Qualifiers  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1  
Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,  
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,  
Pooni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.  
and Ye, W.  
Compositions and methods for the diagnosis and treatment of  
disorders involving angiogenesis  
Patent: WO 0200690-A 29 03-JAN-2002;  
Genentech, Inc. (US)

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mRNA, complete cds.
VERSION AY029191
KEYWORDS AY029191.1 GI:16151084
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Yamada,S., Murakami,S., Matoba,R., Ozawa,Y., Yokokoji,T.,
Nakahira,Y., Ikezawa,K., Takayama,S., Matsubara,K. and Okada,H.
Expression profile of active genes in human periodontal ligament
and isolation of PLAP-1, a novel SLRP family gene
Gene 275 (2), 279-286 (2001)
11587855
PUBMED 21472263
2 (bases 1 to 2466)
Yamada,S., Murakami,S., Matoba,R., Matsubara,K. and Okada,H.
Direct Submission
Submitted (03-APR-2001) Department of Periodontology, Osaka
University Graduate School of Dentistry, 1-8 Yamadaoka, Suita,
Osaka 565-0871, Japan
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RESULT 6  
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DEFINITION Homo sapiens CDNA FLJ20129 fis, clone COL06190.  
ACCESSION AK000136  
VERSION AK000136.1 GI:7020026  
KEYWORDS oligo capping; fis (full insert sequence).  
SOURCE Homo sapiens colon CDNA to mRNA, clone\_lib:COL clone:COL06190.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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REFERENCE  
1 (sites)  
Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y.,  
Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,  
Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.  
NEDO human cDNA sequencing project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1903)  
Sugano,S., Tanaka,T. and Nakamura,Y.  
Shibahara,T., Tanaka,T., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,  
Direct Submission  
Submitted (15-FEB-2000) Sumio Sugano, Institute of Medical Science,  
University of Tokyo, Department of Virology, Shirokane-dai, 4-6-1,  
Minato-ku, Tokyo 108-8639, Japan (E-mail:cdna@ims.u-tokyo.ac.jp,  
Tel:81-3-5449-5286, Fax:81-3-5449-5416)  
NEDO human cDNA sequencing project supported by Ministry of  
International Trade and Industry of Japan; cDNA full insert  
sequencing: Research Association for Biotechnology; cDNA library  
construction, 5'- & 3'-end one pass sequencing: Department of  
Virology and Human Genome Center, Institute of Medical Science,  
University of Tokyo (partly supported by Science and Technology  
Agency). Location/Qualifiers









Best Local Similarity 99.7%; Pred. No. 8.3e-223;  
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DEFINITION Homo sapiens asporin precursor (ASPN) mRNA, complete cds.
ACCESSION AF316824
VERSION AF316824.1 GI:13625796
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1184)
AUTHORS Lorenzo P., Asperg, A., Onnerfjord, P., Bayliss, M.T., Neame, P.J. and
Heinegard, D.
TITLE Identification and characterization of asporin, a novel member of
the leucine-rich repeat protein family closely related to decorin
and biglycan
JOURNAL J. Biol. Chem. 276 (15), 12201-12211 (2001)
MEDLINE 21192276
PUBMED 11152692
REFERENCE 2 (bases 1 to 1184)
AUTHORS Asperg, A.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-2000) Cell and Molecular Biology, Lund
University, BMC plan C12, Lund SE-221 84, Sweden
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RESULT 12  
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DEFINITION Sequence 162 from Patent W00157058.  
ACCESSION AX210520  
VERSION AX210520.1 GI:15424780  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 496)  
AUTHORS Rosenthal, A., Hinzmann, B., Schaefer, R., Zuber, J., Tchernitsa, O., Grips, M., Hellriegel, M., Schmitz, A.C. and Sers, C.  
TITLE Detection of differential gene expression  
JOURNAL Patent: WO 0157058-A 162 09-AUG-2001;  
Metagen Gesellschaft fuer Genomforschung mbH (DE)  
FEATURES  
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AF247821.1 GI:11761718  
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Oreochromis niloticus  
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Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;  
Labroidae; Cichlidae; Oreochromis.  
REFERENCE 1 (bases 1 to 1634)  
AUTHORS Shintani, S., Sato, A., Toyosawa, S., O'higgin, C. and Klein, J.  
TITLE Biglycan-like extracellular matrix genes of agnathans and teleosts  
JOURNAL J. Mol. Evol. 51 (4), 363-373 (2000)  
MEDLINE 20496956  
PUBMED 11040287  
REFERENCE 2 (bases 1 to 1634)  
AUTHORS Shintani, S.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAR-2000) Abteilung Immunogenetik,  
Max-Planck-Institut fur Biologie, Corrensstr. 42, Tubingen  
D-72076, Germany  
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Db      870  CTGGGCGCATTTGATGCTTGAAGCTGAAGTACTTGCCTGTTTCCGAGGCAAACTGTCG 929
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1231  CAACAGTGCACAAAGATGAGAAATCTTTATACAGTGCATTAAGTTTATTCACAAACCCG 1290
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  INITIATION
  SEQUENCE, 5 unordered pieces.
AC123954
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  VERSION   2
  KEYWORDS  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
  SOURCE    house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 263505)
            McPherson,J.D. and Waterston,R.H.
            The sequence of Mus musculus, clone
            Unpublished
            2 (bases 1 to 263505)
            McPherson,J.D. and Waterston,R.H.
            Direct Submission
            Title
            Submitted (05-JUN-2002) Genome Sequencing Center, 4444 Forest Park
            Parkway, St. Louis, MO 63108, USA
            3 (bases 1 to 263505)
            McPherson,J.D. and Waterston,R.H.
            Direct Submission
            Title
            Submitted (12-JUN-2002) Genome Sequencing Center, 4444 Forest Park
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## COMMENT

Parkway, St. Louis, MO 63108, USA  
On Jun 12, 2002 this sequence version replaced gi:21326414.

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
Contact: submissions@watson.wustl.edu  
----- Project Information -----  
Center project name: M\_BA0249L06

## ----- Summary Statistics -----

Sequencing vector: p13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-terminator ET; 0% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 260453 bases at least Q40  
Consensus quality: 261297 bases at least Q30  
Consensus quality: 261814 bases at least Q20  
Insert size: 191000; agarose-fp  
Insert size: 262986; sum-of-contigs  
Quality coverage: 19.29 in Q20 bases; agarose-fp  
Quality coverage: 10.67 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

\* 1 119: contig of 119 bp in length  
\* 120 219: gap of unknown length  
\* 220 25103: contig of 24884 bp in length  
\* 25203: gap of unknown length  
\* 25204 61614: contig of 36411 bp in length  
\* 61615 97169: gap of unknown length  
\* 97170 97269: contig of 35455 bp in length  
\* 97270 263505: contig of 166236 bp in length.

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Best Local Similarity 64.8%; Pred. No. 1.9e-51;  
Matches 757; Conservative 0; Mismatches 282; Indels 129; Gaps 13;

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Job time : 6346 secs

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QY	1473	CAAAATATCTATTCCTCAAGTGGTAAGTCCCACTGACTTATTTTATGACAGAATAATTTCAACG	1532
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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 09:47:27 ; Search time 556 Seconds  
(without alignments)  
9939.575 Million cell updates/sec

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Perfect score: 2454  
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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Matched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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2	2454	100.0	2454	22	Human cDNA sequenc
3	2454	100.0	2454	24	Human angiogenesis
4	2454	100.0	2454	20	Human PRO241 cDNA
5	2443	99.6	2455	21	Human PRO241 cDNA
6	1786.8	72.8	2089	22	Human cDNA sequenc
7	1524	62.1	1674	22	Human encoding human
8	1427.4	58.2	1548	22	Human polynucleoti
9	1288.8	52.5	1492	23	DNA encoding novel

10	1254.8	51.1	18595	22	AAS33411	DNA encoding human
11	1136.6	46.3	2305	24	ABL10114	Mouse bone/cartila
12	1136.6	46.3	2305	24	ABL35045	Murine cDNA isolat
13	790.2	32.2	896	22	AAI94377	Human neuroblastom
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15	774.8	31.6	854	22	AAH16847	Human cDNA clone (
16	614	25.0	899	22	AAI94378	Human neuroblastom
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19	496.6	20.2	574	22	AH16901	Human cDNA clone (
20	462	18.8	496	22	AH81653	Human differential
21	328	13.4	330	20	AAH1488	Human secreted pro
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23	295.4	12.0	1002	14	AAQ50046	Mature decorin pr-
24	295.4	12.0	1026	17	AAT10741	Human recombinant
25	295.4	12.0	1837	20	AZ41383	Human normal uteru
26	295.4	12.0	2063	23	ABV22279	Human prostate exp
27	295.4	12.0	2063	23	ABV24765	Human prostate exp
28	295.4	12.0	2063	23	ABV26594	Human prostate exp
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30	295.4	12.0	2063	23	ABV28779	Human normal ovari
31	295.4	12.0	2078	20	AZ41275	DNA encoding novel
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34	295.4	12.0	4192	17	AAT16517	Human DNA encoding
35	294.6	12.0	1685	22	AAD07372	Human biglycan enc
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39	294.6	12.0	1685	24	ABL64383	Human cDNA encodin
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44	291.4	11.9	1685	24	AAQ04490	Human prostate exp
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#### ALIGNMENTS

#### RESULT 1

AXX80043  
ID AXX80043 standard; cDNA; 2454 BP.

AXX80043;

12-AUG-1999 (first entry)

Human PRO241 nucleotide sequence.

Human; PRO protein; tumour necrosis factor family; TNF; cytokine;  
secreted protein; transmembrane protein; inflammation disorder; ss.

Homo sapiens.

WO9928462-A2.

10-JUN-1999.

01-DEC-1998; 98WO-US25108.

25-FEB-1998; 98US-0075945.

03-DEC-1997; 97US-0067411.

11-DEC-1997; 97US-0069278.

11-DEC-1997; 97US-0069334.

11-DEC-1997; 97US-0069335.

12-DEC-1997; 97US-0069425.

16-DEC-1997; 97US-0069694.

16-DEC-1997; 97US-0069696.

17-DEC-1997; 97US-0069702.

17-DEC-1997; 97US-0069870.

17-DEC-1997; 97US-0069873.

PR 18-DEC-1997; 97US-0068017.  
PR 05-JAN-1998; 98US-0070440.  
PR 09-FEB-1998; 98US-0074086.  
PR 09-FEB-1998; 98US-0074092.  
XX (GETH ) GENENTECH INC.  
XX  
XX Baker KP, Chen J, Goddard A, Gurney AL, Wood WI;  
PI Yuan J;  
XX  
XX WPI: 1999-371118/31.  
DR P-PSDB; AAY17820.  
XX  
XX Nucleic acids encoding PRO secreted and transmembrane proteins  
XX  
XX Claim 2; Fig 1; 123pp; English.  
XX  
XX The present invention describes nucleic acids encoding PRO secreted and  
CC transmembrane proteins used therapeutically. The PRO proteins have  
CC cytosolic, anti-inflammatory, anti-proliferative and immunosuppressive  
CC activity. The proteins and polynucleotides can be used in therapy.  
CC identification of homologues, raising antibodies and design of probes  
CC and primers. They can be used in a range of diseases related to proteins  
XX that they have homology with, e.g. a PRO protein having homology to  
XX complement proteins may be used in inflammatory responses.  
XX  
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Qy 1621 AATCTCATGCTTGACCATCTCCTTTCTTCATAAACAAGTAAGATATCGGTATTTAAC 1680  
Db 1621 AATCTCATGCTTGACCATCTCCTTTCTTCATAAACAAGTAAGATATCGGTATTTAAC 1680  
Qy 1681 ACTTTGTTATCAAGCACATTTTAAAGAACTGTACTGTAAATGGAATGCTTGACTTAGC 1740  
Db 1681 ACTTTGTTATCAAGCACATTTTAAAGAACTGTACTGTAAATGGAATGCTTGACTTAGC 1740

Db 1681 ACTTTGTTATCAAGCACATTTTAAAGAAAGTACTCTAAATGAATGCTTGACTAGC 1740  
QY 1741 AAAATTTGCTGCTTTTCATTTGCTCTTAGAAAACAGAAATTAACAAACACAGTAAATGTA 1800  
Db 1741 AAAATTTGCTGCTTTTCATTTGCTCTTAGAAAACAGAAATTAACAAACACAGTAAATGTA 1800  
QY 1801 AGAGTGCAATACACTATTCTTTATTTCTTTAGTAACTGGGTAGTACTGTAATATTTTAAAT 1860  
Db 1801 AGAGTGCAATACACTATTCTTTATTTCTTTAGTAACTGGGTAGTACTGTAATATTTTAAAT 1860  
QY 1861 CATCTTAAAGTATGATTTGATATATATCTTTATTTGAAATTTACCTTATCATGCTTAGAGCCC 1920  
Db 1861 CATCTTAAAGTATGATTTGATATATATCTTTATTTGAAATTTACCTTATCATGCTTAGAGCCC 1920  
QY 1921 GTCCTTATGTTTAAACCTAAATTTCTTAAATAAAGCCCTTCAGTAAATGTTCAATACCAAC 1980  
Db 1921 GTCCTTATGTTTAAACCTAAATTTCTTAAATAAAGCCCTTCAGTAAATGTTCAATACCAAC 1980  
QY 1981 TTGATAAATGCTACTCATAAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040  
Db 1981 TTGATAAATGCTACTCATAAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040  
QY 2041 ATTATACCTGATTTAAATCTCTGTAAACGCTGTAGTGTTCATAAATCTGTAAT 2100  
Db 2041 ATTATACCTGATTTAAATCTCTGTAAACGCTGTAGTGTTCATAAATCTGTAAT 2100  
QY 2101 CGCATTTTAAATGCTCTATATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160  
Db 2101 CGCATTTTAAATGCTCTATATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160  
QY 2161 ACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGGCTG 2220  
Db 2161 ACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGGCTG 2220  
QY 2221 GAAGAGCTGGACACTACAATCTACACCAATTTCTCTTCAATAGCTATGACTGG 2280  
Db 2221 GAAGAGCTGGACACTACAATCTACACCAATTTCTCTTCAATAGCTATGACTGG 2280  
QY 2281 ATAACTCTGAGAAACACATCTAGTAACTGAATGAAGAGACATCAAAATTAACAGACA 2340  
Db 2281 ATAACTCTGAGAAACACATCTAGTAACTGAATGAAGAGACATCAAAATTAACAGACA 2340  
QY 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGTTATTTCTTATTTGGCATTCAA 2400  
Db 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGTTATTTCTTATTTGGCATTCAA 2400  
QY 2401 CATATGTAATTCAGAAACAGGGAAATTTTCATTAATAATATGTTTGAAT 2454  
Db 2401 CATATGTAATTCAGAAACAGGGAAATTTTCATTAATAATATGTTTGAAT 2454

RESULT 2

AA521407  
ID AAS21407 standard; cDNA; 2454 BP.  
XX AAS21407;  
AC AAS21407;  
XX AAS21407;  
DT 24-OCT-2001 (first entry)  
XX Human cDNA sequence encoding for PRO241 polypeptide.  
DE Human secretory and transmembrane; PRO; mammalian; cancer; lung;  
KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;  
KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;  
KW adipocyte; A-peptide; factor VIIA; gene therapy; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX WO200140466-A2.  
PN WO200140466-A2.  
XX 07-JUN-2001.  
PD 07-JUN-2001.  
XX 01-DEC-2000; 2000WO-US32678.

XX 01-DEC-1999; 99WO-US28301.  
PR 01-DEC-1999; 99WO-US28634.  
PR 02-DEC-1999; 99WO-US28551.  
PR 02-DEC-1999; 99WO-US28564.  
PR 02-DEC-1999; 99WO-US28565.  
PR 09-DEC-1999; 99US-0170262.  
PR 16-DEC-1999; 99WO-US30095.  
PR 20-DEC-1999; 99WO-US30911.  
PR 20-DEC-1999; 99WO-US30999.  
PR 30-DEC-1999; 99WO-US31243.  
PR 06-JAN-2000; 2000WO-US00277.  
PR 06-JAN-2000; 2000WO-US00376.  
PR 11-FEB-2000; 2000WO-US03565.  
PR 18-FEB-2000; 2000WO-US04341.  
PR 18-FEB-2000; 2000WO-US04342.  
PR 22-FEB-2000; 2000WO-US04414.  
PR 24-FEB-2000; 2000WO-US04914.  
PR 24-FEB-2000; 2000WO-US05004.  
PR 01-MAR-2000; 2000WO-US05601.  
PR 20-MAR-2000; 2000WO-US07377.  
PR 21-MAR-2000; 2000WO-US07532.  
PR 30-MAR-2000; 2000WO-US08439.  
PR 17-MAY-2000; 2000WO-US13705.  
PR 22-MAY-2000; 2000WO-US14042.  
PR 30-MAY-2000; 2000WO-US14941.  
PR 02-JUN-2000; 2000WO-US15264.  
PR 10-NOV-2000; 2000WO-US30873.  
XX (GETH ) GENENTECH INC.  
PA Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;  
Gerritsen ME, Goddard A, Godowski RJ, Gurney AL, Sherwood S;  
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;  
XX WPI; 2001-408281/43.  
DR P-PSDB; AAU12335.  
XX Isolated, secretory and transmembrane PRO polypeptide used to detect  
other PRO polypeptides, link bioactive molecules to cells expressing  
PRO polypeptides, and detect the presence of mammalian tumours e.g.  
lung, breast, prostate, cervical  
Claim 3; Fig 327; 813pp; English.  
XX AAS21244-AAS21518 encode for novel human secretory and transmembrane  
PRO polypeptides. The PRO polypeptides are useful to detect other  
PRO polypeptides, to link bioactive molecules to cells expressing  
PRO polypeptides, to modulate biological activities of cells expressing  
PRO polypeptides, and to detect the presence of mammalian lung, colon,  
breast, prostate, rectal, cervical or liver tumours by comparing PRO  
polypeptide expression in a cell sample to that in a control sample.  
Some of the 275 sequences are also useful to stimulate the release of  
tumour necrosis factor-alpha (TNF-alpha) from human blood, the  
proliferation or differentiation of chondrocytes, the proliferation or  
gene expression in pericyte cells, the release of proteoglycans from  
cartilage, the proliferation of inner ear utricular supporting cells or  
of T-lymphocytes, the release of a cytokine from peripheral blood  
monocytes (PBMCs), or the proliferation of endothelial cells. Some of  
the PRO polypeptides may modulate glucose or free fatty acid uptake by  
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide  
to factor VIIA. The PRO polypeptides can be used in assays to identify  
molecules involved in binding interactions. The polynucleotides encoding  
PRO polypeptides can be used to generate probes, antisense RNA/DNA,  
transgenic or knock out animals and can be used in gene therapy.  
XX Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;  
SQ

Query Match 100.0%; Score 2454; DB 22; Length 2454;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGACATATCTGTGGAGCAGTATTATCCAGTATACCCAGGTGCAGCCACAGGACT 60







301 ACATCCACTGAAGATATGATGCTGAAGCATATGGAAGACACAGATGATGATGATG 360  
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
421 GCATTTTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
421 GCATTTTTCATTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 480  
481 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
481 GAGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 540  
541 CTCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
541 CTCGAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 600  
601 GACTCACTTCACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
601 GACTCACTTCACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 660  
661 AGCCCTTTTCACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
661 AGCCCTTTTCACTTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 720  
721 AATATCCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
721 AATATCCACTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 780  
781 AGAAATACAAAGGACACATTTCAAGGAATGATGATGATGATGATGATGATGATG 840  
781 AGAAATACAAAGGACACATTTCAAGGAATGATGATGATGATGATGATGATGATG 840  
841 CAAACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
841 CAAACCTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 900  
901 ATATCAGAAATGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 960  
901 ATATCAGAAATGAGAGGCTGATGATGATGATGATGATGATGATGATGATGATG 960  
961 TGAGCTTCACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
961 TGAGCTTCACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020  
1021 ACAGAACTACAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
1021 ACAGAACTACAAAGGCTGATGATGATGATGATGATGATGATGATGATGATGATG 1080  
1081 GTCTTCTTACATACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
1081 GTCTTCTTACATACCACTGATGATGATGATGATGATGATGATGATGATGATGATG 1140  
1141 TCCCTTCACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
1141 TCCCTTCACTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1200  
1201 TTGCAAGCTGGAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1260  
1201 TTGCAAGCTGGAGTAAATGATGATGATGATGATGATGATGATGATGATGATGATG 1260  
1261 ACAGTGAATAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
1261 ACAGTGAATAGTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1320  
1321 TTCGTTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
1321 TTCGTTGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1380  
1381 TAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440  
1381 TAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1440

RESULT 4  
ABL88086  
ID ABL88086 standard; cDNA; 2454 BP.

1441 TCTATTAATAATGCTAGTATTATATATACAAAGCAATATCTATTCTCAAGTGTGTAAGTCC 1500  
1441 TCTATTAATAATGCTAGTATTATATATACAAAGCAATATCTATTCTCAAGTGTGTAAGTCC 1500  
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTTCCGCAAACTATTGATACATAAG 1560  
1501 ACTGACTTATTTTATGACAGAAATTTCAACGGAATTTTCCGCAAACTATTGATACATAAG 1560  
1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTCCGCTACAAATGATCTTACATA 1620  
1561 GGGTTGAGAGAAACAGCATCTATTGCGAGTTTCCCTTTTCCGCTACAAATGATCTTACATA 1620  
1621 AATCTCATGCTTCCACCATTTCTTCTTATACAAAGAAAGTAAAGATATTCGGTATTAAAC 1680  
1621 AATCTCATGCTTCCACCATTTCTTCTTATACAAAGAAAGTAAAGATATTCGGTATTAAAC 1680  
1681 ACTTTGTTATCAAGCACTTTTAAAGAACTGCTACTGTAAGTAAAGTAAAGTAAAGTAAAG 1740  
1681 ACTTTGTTATCAAGCACTTTTAAAGAACTGCTACTGTAAGTAAAGTAAAGTAAAGTAAAG 1740  
1741 AAAATTTGCTCTTTTCACTTTGCTGTAGAAAACAGAAATTAACAAGACAGTAATGTGA 1800  
1741 AAAATTTGCTCTTTTCACTTTGCTGTAGAAAACAGAAATTAACAAGACAGTAATGTGA 1800  
1801 AGAGTGCACTTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860  
1801 AGAGTGCACTTACACTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1860  
1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTTACCTTTATCATGCTTTAGAGCCC 1920  
1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTTACCTTTATCATGCTTTAGAGCCC 1920  
1921 GTCCTTATGTTTAAAGCACTTTTCTTAAATAAGGCTTCAAGTAAATGTTTCAATACCAAC 1980  
1921 GTCCTTATGTTTAAAGCACTTTTCTTAAATAAGGCTTCAAGTAAATGTTTCAATACCAAC 1980  
1981 TTGATAAATGCTACTCATAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTCTTTT 2040  
1981 TTGATAAATGCTACTCATAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTCTTTT 2040  
2041 ATTATTACCTGATTTTAAAAATCTCTGTAAGAACTGCTAGTGTGTTTCTTATAAAATCTGTA 2100  
2041 ATTATTACCTGATTTTAAAAATCTCTGTAAGAACTGCTAGTGTGTTTCTTATAAAATCTGTA 2100  
2101 CGCATTTTATGATGCTGCTTATTAAGCTTTTAAATAGCATGAAAATGTTTAGGCTATATA 2160  
2101 CGCATTTTATGATGCTGCTTATTAAGCTTTTAAATAGCATGAAAATGTTTAGGCTATATA 2160  
2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGGAGAGCTTCTGTTG 2220  
2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGGAGAGCTTCTGTTG 2220  
2221 GAAGAGCTTGGACACTTAAACAAATTTCTACCAAAATTTCTCTTCAAAATACGTATGGACTGG 2280  
2221 GAAGAGCTTGGACACTTAAACAAATTTCTACCAAAATTTCTCTTCAAAATACGTATGGACTGG 2280  
2281 ATAACCTCTGAGAAACACATCTAGTATACTGAATAGAGAGAGCATCAAAATTAACAGACA 2340  
2281 ATAACCTCTGAGAAACACATCTAGTATACTGAATAGAGAGAGCATCAAAATTAACAGACA 2340  
2341 GAAACGGAAGCTCTATATAAATGCTCAGAGTTCTTTTATGTTTCTTATTTGTCATTTCAA 2400  
2341 GAAACGGAAGCTCTATATAAATGCTCAGAGTTCTTTTATGTTTCTTATTTGTCATTTCAA 2400  
2401 CATATCTAAAATCAGAAAAACAGGAAATTTTTCATTAAAAATATTTGTTTGAAT 2454  
2401 CATATCTAAAATCAGAAAAACAGGAAATTTTTCATTAAAAATATTTGTTTGAAT 2454



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Db 721 AATACCCTTAATCTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAATAAAGTTA 780
Qy 781 AGAAATACAAAGACACATTCAAAGGAATGCTTTACACGCTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGACACATTCAAAGGAATGCTTTACACGCTTTGGAAATGAGTG 840
Qy 841 CAACCCCTCTTGATTAATATGAGATAGACAGGCGCAATTTCAAGGGGTGACGGTGTCC 900
Db 841 CAACCCCTCTTGATTAATATGAGATAGACAGGCGCAATTTCAAGGGGTGACGGTGTCC 900
Qy 901 ATATCAGAATTCGAGAAGCAAACTGACCTCAGTTTCCCTAAAGGCTTACCAACCACTTAT 960
Db 901 ATATCAGAATTCGAGAAGCAAACTGACCTCAGTTTCCCTAAAGGCTTACCAACCACTTAT 960
Qy 961 TGGAGCTTCACCTAGATATATATAAATTTCAACAGTGGAACTTCAGGATTTTAAACGAT 1020
Db 961 TGGAGCTTCACCTAGATATATATAAATTTCAACAGTGGAACTTCAGGATTTTAAACGAT 1020
Qy 1021 ACAAGAACTACAAAGGCTGGGCTTGGGAAACAAACAAATACAGATATCGAAATGGGA 1080
Db 1021 ACAAGAACTACAAAGGCTGGGCTTGGGAAACAAACAAATACAGATATCGAAATGGGA 1080
Qy 1081 GTCCTGCTAACATACCACTGCTGAGAGAAATACATTTGGGAAACAAATACCACTTAAACAAA 1140
Db 1081 GTCCTGCTAACATACCACTGCTGAGAGAAATACATTTGGGAAACAAATACCACTTAAACAAA 1140
Qy 1141 TCCCTTCAGGATTCACAGATGGAATACCTCCAGATATCTTCCCTCATCTAATTTCAA 1200
Db 1141 TCCCTTCAGGATTCACAGATGGAATACCTCCAGATATCTTCCCTCATCTAATTTCAA 1200
Qy 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCACACAGTCCCAAGATGAAGAACTCTTAT 1260
Db 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCACACAGTCCCAAGATGAAGAACTCTTAT 1260
Qy 1261 ACAGTSCAATAAGTTTATTCACAAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
Db 1261 ACAGTSCAATAAGTTTATTCACAAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320
Qy 1321 TTCGTTGGTTTGGAGCAGATGAGTGTTCAGCTTGGGAACCTTGGAAATGAATTAATAG 1380
Db 1321 TTCGTTGGTTTGGAGCAGATGAGTGTTCAGCTTGGGAACCTTGGAAATGAATTAATAG 1380
Qy 1381 TAATTTGGTAATCTCCATTTAATATAGATTCACAAATCCCTACATTTGGAATACCTTGAAC 1440
Db 1381 TAATTTGGTAATCTCCATTTAATATAGATTCACAAATCCCTACATTTGGAATACCTTGAAC 1440
Qy 1441 TCTATTAAATAGTGTAGTATTATATATACAGCAATATCTTCTCAAGTGGTAAAGTCC 1500
Db 1441 TCTATTAAATAGTGTAGTATTATATATACAGCAATATCTTCTCAAGTGGTAAAGTCC 1500
Qy 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCGCAAACTATTGATACATAG 1560
Db 1501 ACTGACTTATTTATGACAGAAATTTCAACGGAAATTTGCGCAAACTATTGATACATAG 1560
Qy 1561 GGGTTGAGAGAAACAGATCTTATGCGAGTTCCTTTTGGCTACAAATGATCTTACATA 1620
Db 1561 GGGTTGAGAGAAACAGATCTTATGCGAGTTCCTTTTGGCTACAAATGATCTTACATA 1620
Qy 1621 AATCTCATGCTTGACCATTCCTTTCTCATACAAAAAAGTAAGATATTCGGTATTTAAC 1680
Db 1621 AATCTCATGCTTGACCATTCCTTTCTCATACAAAAAAGTAAGATATTCGGTATTTAAC 1680
Qy 1681 ACTTTGTTATCAGCAGATTTTAAAGACGTGACTGTAAATGGAATGCTTGACTTAGC 1740
Db 1681 ACTTTGTTATCAGCAGATTTTAAAGACGTGACTGTAAATGGAATGCTTGACTTAGC 1740
Qy 1741 AAAATTTGCTCTTTCTATTTCTGCTGTAGAAAAACAGAAATTAACAAAGACGATATGCA 1800
Db 1741 AAAATTTGCTCTTTCTATTTCTGCTGTAGAAAAACAGAAATTAACAAAGACGATATGCA 1800
Qy 1801 AGAGTGCAATACACATTTCTTATTTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT 1860
Db 1801 AGAGTGCAATACACATTTCTTATTTCTTTAGTAACCTGGGTAGTACTGTAATATTTTAAAT 1860
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Qy 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTATCATGTCTTAGAGCCC 1920
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTATCATGTCTTAGAGCCC 1920
Qy 1921 GTCCTTATGTTTAAAGCACTAATTTCTTAAATTTAAAGCCCTTCAGTAAATGCTTCAATACCAAC 1980
Db 1921 GTCCTTATGTTTAAAGCACTAATTTCTTAAATTTAAAGCCCTTCAGTAAATGCTTCAATACCAAC 1980
Qy 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Db 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATGCTTTTTTTTTTTA 2040
Qy 2041 ATTATTACCTCATTTAAATCTCTGTAAACCTGTAGTCTTTCATAAAATCTGTAAT 2100
Db 2041 ATTATTACCTCATTTAAATCTCTGTAAACCTGTAGTCTTTCATAAAATCTGTAAT 2100
Qy 2101 CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTAGGCTATATA 2160
Db 2101 CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTAGGCTATATA 2160
Qy 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGTG 2220
Db 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGTG 2220
Qy 2221 GAAGAGCTGACACTACAAATTTACACCAAAATTTCTTCAAAATGCTCTTCAAAATGCTGACTGG 2280
Db 2221 GAAGAGCTGACACTACAAATTTACACCAAAATTTCTTCAAAATGCTCTTCAAAATGCTGACTGG 2280
Qy 2281 ATAACCTGAGAAACACATCTAGTATATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACCTGAGAAACACATCTAGTATATACTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Qy 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTATGATTTCTTTATGGCAATCAA 2400
Db 2341 GAAACCGAAGCTCTATATAAATGCTCAGAGTCTTTATGATTTCTTTATGGCAATCAA 2400
Qy 2401 CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATGGTTTGAAT 2454
Db 2401 CATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATGGTTTGAAT 2454
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## RESULT 5

AAA49551  
ID AAA49551 standard; cDNA; 2455 BP.

XX AAA49551;

XX 25-SEP-2000 (first entry)

XX Human PRO241 cDNA.

XX PRO; membrane bound protein; secreted protein; PRO357; PRO327;  
KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;  
KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;  
KW antibody; screening; detection; inhibition; probe; primer; human;  
KW ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH CDS 234..1373

FT /\*tag= a  
FT /product= PRO241 polypeptide

XX WO200032776-A2.

XX 08-JUN-2000.

XX 01-DEC-1999; 99WO-US28301.

XX 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.





















compounds, to quantitatively determine levels of interacting proteins or other compounds, and as therapeutic target in a whole range of disease states. Compositions comprising the novel proteins of the invention are useful for treating mammalian disorders. Polynucleotides of the invention are useful in genome and physical mapping, in positional cloning of genes, to tag or identify an organism or its reproductive material (as non-disruptive tags for marking organisms), and for the diagnosis and treatment of mammalian diseases which is the consequence of inappropriate expression of kinase genes. They are useful for promoting immune response as part of a vaccine or anti-cancer treatment, as target for cancer treatment, as immunoregulatory and anti-inflammatory molecule, as diagnostic for specific types of cancer and for development of an anti-cancer treatment, and as a target for antagonists in the treatment of diseases such as asthma and allergy. They are also useful to inhibit or enhance the activity of the soluble molecule that binds proteins of the invention, for tissue and neural regeneration, to promote or block cell trafficking, and as anti-inflammatory and/or vaccine adjuvant. The present sequence is a cDNA encoding bone/cartilage proteoglycan I protein (BGN), a secreted protein from mouse. BGN is also known as biglycan or PG-S1.

XX Sequence 2305 BP; 809 A; 395 C; 391 G; 710 T; 0 other;

Query Match 46.3%; Score 1136.6; DB 22; Length 2305;

Best Local Similarity 74.3%; Pred. No. 2e-228;

Matches 1747; Conservative 0; Mismatches 434; Indels 170; Gaps 18;

QY	6	AATCTGTGGGACAGTTTATTCAGTATCACCAGGTCAGCCACACAGGACTGTGTT	65
DB	2	AATCTGTGAAGCAGTTTATTCAGTATCACCAGGA-GCAGCCACACAGAGGCTGGTAG	60
QY	66	GAAGGTG-----TTTTTTTCTTTTAAATGTAATACCTCTCATCTTT	109
DB	61	GAGGCTGAGTTTGTCTCTTTTCTTTTAAATGTAATGTAATGTAATGTAATTTT	120
QY	110	TCTTCTTACACAGTGTCTGAGAACATTTACATATATAGTAAGTACATGTGGATAAC	169
DB	121	TCTTCTTGAAGAGTCT-TGAGGATACCTACATTTGCAAGTTAAGTAGTACAGGTTGATAA	179
QY	170	TTCCTACTTTAGAGAGCTACTCTCTTCAGAGTCCCTAGAGTGGTCTTCTACACTAAGA	229
DB	180	TTCTACTTTGAAGAAATCTCTCTCTGCAAGGTTGGAGTTGTACAC-----AGGC	233
QY	230	CACCTGAAGGAGTAGTCTCTATATTTCTTGGCTTTGTCTGCGCAAAACCTTCTT	289
DB	234	CAGCATGAAGGAGTAGTGTGCTACTGCTTTGGCTGTGTCTGCGCAAAACCTTCTT	293
QY	290	TAGCCCTTCCACACATCGCCTGAAGAAATATGATGCTGAAGGATATGGAAGACAGATGA	349
DB	294	TAGCCCTTCCACACAGCTGAAGAAATATGATGTTGAAGGATATGGAAGACACA-----	348
QY	350	TGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	409
DB	349	-----GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	395
QY	410	AGAGCAAGAGAGCATTCTTTCATTTGATCTGTTTCCAAATGTCGTCATTTGGAGTCA	469
DB	396	AGAGCAGTGAACCTTTTTCCTTTCGATTTGTTTCCAAATGTCGTCATTTGGAGTCA	455
QY	470	GTGCTATTCCAGAGTTGTGATGCTCAGATTTAGCTTTGACCTCAGTCCCAACCAACAT	529
DB	456	ATGTTACTCTGAGTTGTTCACTGCTCTGATCTAGTCTGACATCGTTTCCAAACCAAT	515
QY	530	TCAATTTGATCTGCAATGCTGATCTTCAAAACAATAAATTAAGAAATCAAGAAATA	589
DB	516	TCCATTTGATCTGCAATGCTGATCTTCAAAACAATAAATTAAGAAATCAAGAAATA	575
QY	590	TGATTTTAAGGACTCATTCTCATTGCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	649
DB	576	TGACTTTTAAGGACTCATTCTCATTGCTGATCTGATCTGATCTGATCTGATCTGATCTGAT	635
QY	650	GATTCACCAAAAGCCTTTCTAACCAACAAGAGTTGCGAAGGCTGTATCTGTGCCACAA	709

DB	636	GATTCACCAAAACCTTTCTTACCAACAAGAAATTTAGAGAGCTATATTTATCCACAA	695
QY	710	TCAACTAAGTGAATACCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGA	769
DB	696	CCAACCTAAGTGAATTTCCACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGA	755
QY	770	AAATAAGTTAAGAAATACAAAGGACACATTTCAAAGGAATGAATGCTTTTACACCTTTT	829
DB	756	TAATAAGTTAAGAAATACAAAGGACACGTTTCAAGGGAATGAATGCTTTTACATCTTTT	815
QY	830	GGAAATGAGTGCAAACCTTCTTGATTAATATGATGATAGCCAGGCGCATTTGAAGGGCT	889
DB	816	GGAAATGAGTGCAAACCTTCTTGAGAACACAGGGAAGAGAGAGGCGCATTTGAAGGGCT	875
QY	890	GACGGTGTCCCATATCAGAATTCAGAAGCAAACTGACCTCAGTGTCTTAAAGCTTACC	949
DB	876	GACATGTTTCCCATATCAGGATCCTGAAGCAAACTAACCTCAATTCCAAAGGCTTACC	935
QY	950	ACCACTTTATTTGGAGCTTCTACATTTAGATTAATAAATTTTCAACAGTGGAACTTGA	1009
DB	936	ACCACTTTTGTGTGAGCTTCTTATTAATAAATTTTCAACGCTGGAAGCTTGAAGA	995
QY	1010	TTTAAACGATACAAAGCACTACAAAGGCTGGCGCTAGGAAACAACAATAATCACAGAT	1069
DB	996	TTTAAACGATACAGGGAAGCTGCAAGGCTGGGCTTTGGAAACAACAATAATCACAGAT	1055
QY	1070	CGAAATGGGAGTCTTCTTAACATACACAGTGTGAGAGAAATACATTTGGAACAATAA	1129
DB	1056	TGAATGGAACCTTTTGTCTAATATACACGCTGTGAGAGATACACTTTGGAACAATAA	1115
QY	1130	ACTAAAAAAATCCCTTACAGGATTCACAGTGTGAATACCTCCAGATATCTTCTTCA	1189
DB	1116	ACTAAAAAAATCCCTTACAGGATTCACAGGATTTGAATACTCCAGATATCTTCTTCA	1175
QY	1190	TTCTAATTCATTTGCAAGAGTGGAGTAAATGACTTCTGTCACACAGTGCACAGATGA	1249
DB	1176	TTAATAATTCATTTGCAAGAGTGGAGTAAATGACTTCTGTCACACAGTGCACAGATGA	1235
QY	1250	GAAATCTTTATACAGTCAATAAGTTTATTCACAAACCCGCTGAAATCTGGAATGCA	1309
DB	1236	GAAATCTTTATACAGTCAATAAGTTTATTCACAAACCCGCTGAAATCTGGAATGCA	1295
QY	1310	ACCTGCAACATTTCTGTTGTGTTTGTGAGCAGAAATGAGTGTTCAGCTTGGAACTTGAAT	1369
DB	1296	ACCTGCAACATTTCTGTTGTGTTTGTGAGCAGAAATGAGTGTTCAGCTTGGAACTTGAAT	1354
QY	1370	GTAAATTAATGATTTGGTAAATGTCCATTTAATAATAGATTCAAAATCCCTACATTTGG	1429
DB	1355	-----AATAATTCATGACATCCATTAATAAATTTCAAAAATGTATACATTTGG	1405
QY	1430	AATACTTGAACCTCTATTAAATAGTGTATATATATACAAAGCAAAATATCTATTCTCAA	1489
DB	1406	AATACTTGAACCTCTATTAAATAGTGTATATATATACAAAGCAAAATATCTATTCTCAA	1462
QY	1490	GTGGTAACTCCACTGACTTATTTATGACAGAAATTTCAACGGAATTTTGGCAAACTAT	1549
DB	1463	-----ATATGTCATGACAAAAATTTCAACAGAAATTTTGGCTTAATAT	1507
QY	1550	TGATACATAAGGGGTTGAGAGAAACAGCATCTATTCCAGTGTCTTCTTTCGCTACAAAT	1609
DB	1508	TGATGCTCA-----GAATAAATTTCTATGTCAGTGTCTTCTGACATGATG	1555
QY	1610	GATCTTACATAAATCTCATGCTTGCACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1669
DB	1556	ATCTTTCGCGTAAATCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1610
QY	1670	CGGTATTTTAAACACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1729
DB	1611	TAGTATTTTAAACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1668
QY	1730	CTTGACTTAGCAAAATTTGCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1789
DB	1669	CTTGACTTAGCAAAATTTGCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT	1727



QY 710 TCACTAGTGAATACACCTTAATCTTCCCAATCATATTAGCAGAACCTCAGAAATTCATGA 769  
Db 696 CCAACTAGTGAATTCACCTTAATCTTCCCAATCATATTAGCAGAACCTCAGAAATTCATGA 755  
QY 770 AAATAAGTTAAGAAATACAAAGGACACATCTTCAAGGAATGAATGCTTTACAGCTTTT 829  
Db 756 TAATAAGTTAAGAAATACAAAGGACACATCTTCAAGGAATGAATGCTTTACAGCTTTT 815  
QY 830 GGAATAGTGCACACCTCTTGTATAAATGAATGGGATAGAGCCAGGGCATTTGAAGGGGT 889  
Db 816 GGAATAGTGCACACCTCTTGTAGAACAACGGGATAGAACCGGGCATTTGAAGGGGT 875  
QY 890 GACGGTTTCCATATCAGAAATGCAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACC 949  
Db 876 GACACTATTCCATATCAGAGTCGCTGAAGCAAACTAACCTCAATTCGCAAAAGGCTACC 935  
QY 950 ACCAATTTATGGAGCTTCACTAGATTATATAAATAATCAACAGTGGACTTGAGGA 1009  
Db 936 ACCAATTTGCTGGAGCTTCATTTAGATTATTAATAAATAATCAACGGTGGAACTTTGAAGA 995  
QY 1010 TTTTAAAGCATACAAAGAACTACAAAGGCTGGCCCTAGGAACAACAAATCACAGATAT 1069  
Db 996 TCTTAAAGCATACAAAGAACTACAAAGGCTGGCTTGGAAACAACAGATCACAGATAT 1055  
QY 1070 CGAAATGGAGCTTTGCTTAACATACACAGTGTGAGAGAAATACATTTGGAAAAACAATA 1129  
Db 1056 TGAATGGAAGCTTTGCTTAATATACACAGTGTGAGAGATACACCTTGGAAACAATAA 1115  
QY 1130 ACTAAAAAATCCCTTACAGATTACAGAGTTGAATACCTCCAGATAACTTCTCTTCA 1189  
Db 1116 ACTAAAAAATCCCTTACAGATTACAGAGTTGAATACCTCCAGATAACTTCTCTTCA 1175  
QY 1190 TTCTAATTCATTTGCAAGAGTGGGAGTAAATGACATCTGTCCACAGTGCCAAAGATGAA 1249  
Db 1176 TTATTAATTCATTTGCAAGAGTGGGAGTAAATGACATCTGTCCACAGTGCCAAAGATGAA 1235  
QY 1250 GAAATCTTTATACAGTGCATTAAGTTTATTCACAAACCCGGTGAATATCTGGGAAATGCA 1309  
Db 1236 GAAATCTTTATACAGTGCATTAAGTTTATTCACAAACCCGGTGAATATCTGGGAAATGCA 1295  
QY 1310 ACCTGCAACATTTCTGTTGTTTTCAGCAGATGAGTGTTCAGCTTTGGGAATTTGGGAT 1369  
Db 1296 ACCTGCAACATTTCTGTTGTTTTCAGCAGATGAGTGTTCAGCTTTGGGAATTTGGGAA- 1354  
QY 1370 GTAATAATAGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1429  
Db 1355 -----ATAATTCATGACATCCATTAATATATAAATGTAATGTAATGTAATGTAATGTAAT 1405  
QY 1430 AATACTGAACTCTATTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1489  
Db 1406 AATACTGAACTCTCTAGTAAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAAT 1462  
QY 1490 GTGGTAACTGCACTGCTTTATTTATGACAGAAATTTCAACGGAAATTTTGGCAAACTAT 1549  
Db 1463 -----ATATGTCATGATCAAAATTTTCAACAGAAATTTTGGCAAACTAT 1507  
QY 1550 TGATACATAAGGGTTGAGAGAAACACATCTATTGTCAGTTTCTTTTTCGGTACAAT 1609  
Db 1508 TGATGCTCA-----GAATAAATTTCTATTGTCAGTGTCTCTCTGCAATGAATG 1555  
QY 1610 GATCTTACATAAATCTGCTTGACCATTTCTTTCTTCAATAACAAAGAAATTAAGATATT 1669  
Db 1556 ATTCTTGGTAAATCTTTGCTTGACATCTTTTCTTTTTCGGCAAAA-----AAGATATT 1610  
QY 1670 CGGTATTTAAGCACTTTGTTATCAGCAGATTTTAAAGAAAGTGTACTGTAATGGAATG 1729  
Db 1611 TAGTATTTAAGCACTTTGTTATCAGCAGATTTTAAAGAAAGTGTACTGTAATGGAATG 1668  
QY 1730 CTGACTTACCAAAATTTGCTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1789  
Db 1669 CTGACTTACCAAAATTTGCTCTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1727  
QY 1790 CAGTAATGTAAGAGTGCATTTACACTATTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCT 1846

Db 1728 CAGCACTTTTGAAGAGTACATATATTTTAGTAGTTTAAAAAAGCTTGGACAGTACT 1787  
QY 1847 GTAATATTTTAAATCATCTTAAAGTATGATTTGATATATCTTATTTGAAATTTACCTTATC 1906  
Db 1788 GTAATGTTTCCCAATGTTGGAATACATATAGTTTGAC----- 1826  
QY 1907 ATGTCTTAGAGCCCTCTTTTATGTTTAAACCTAAATTTCTTAAATAAAGCCCTTCAAGTAA 1966  
Db 1827 -----AGAATCAAAATTTCTCAACTCATAATAAAGCTTCAAGTA-- 1864  
QY 1967 TGTTCATTACCAACTTGTATAATGCTACTCATAGAGCTGGTTTGGGGCTATAGCATATG 2026  
Db 1865 -----TTCACAGATAATATTCATCAGAGTTGGTTT--GGGCTATAACACATG 1909  
QY 2027 CTTTCTTTTAAATTTTAACTGATTTAAATACTCTGTAAATACTCTGTAAATACTCTTCA 2086  
Db 1910 ATATCTCTTTTAAATTTTAACTGATTTAAATACTCTGTAAATACTCTGTAAATACTCTTCA 1969  
QY 2087 TAAATCTGTAACCTGCACTTTTAAATGATCCGCTATTATAAGCTTTTAAATGATGAAAT 2146  
Db 1970 TAAATCTGTAACCTGCACTTTTAAATGATCCGCTATTATAAGCTTTTAAATGATGAAAT 2027  
QY 2147 TGTAGGCTATATACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTG 2206  
Db 2028 TGTAGGCTATATACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTG 2083  
QY 2207 GAAGACCTTGTCTTGAAGAGCTGACACATCTTACACCAATTTCTCTCTTCAAA 2266  
Db 2084 GAACAGTATG-----GACGCAATCAATTTTATATCACTTATCTCTTCAAA 2130  
QY 2267 TACGTATGAGCTTGGATACTCTGAGAAACACATCTAGTATTAATCACTGAAAGCAGAGCATC 2326  
Db 2131 TATGACATTTGGTAAATGCTTGAACATAGCTAGTAAAGTGAACAACTGAAACCTGAACT 2190  
QY 2327 AATTAACAG 2337  
Db 2191 AACTTAATAG 2201

## RESULT 13

AA194377  
ID AA194377 standard; cDNA; 896 BP.

XX AA194377;

XX AA194377;

DT 13-NOV-2001 (first entry)

XX Human neuroblastoma expressed polynucleotide SEQ ID NO 452.

DE Human; neuroblastoma; malignancy; cancer; tumour marker; N-myc; TrkA; ss.

OS Homo sapiens.

XX WO200166719-A1.

XX 13-SEP-2001.

PD 02-MAR-2001; 2001WO-JP01629.

PF 07-MAR-2000; 2000JP-0159195.

PR (CHIB-) CHIBA PREFECTURE.

PA (HISM) HISAMITSU PHARM CO LTD.

PI Nakagawara A;

XX WPI; 2001-565584/63.

XX Nucleic acids originating in gene expressed in human neuroblastoma,  
PT useful as probe or primer in diagnosing prognosis of human  
PT neuroblastoma, malignancy and susceptibility indicator or tumour marker  
PT for anti-cancer agents

xx PS Claim 1; Page 377; 2979pp; Japanese.

xx CC The invention relates to novel genes (AAI93926-AAI97963) expressed in human neuroblastoma. The nucleic acids are applicable as a probe or primer in diagnosing the prognosis of human neuroblastoma, malignancy and susceptibility indicators or tumour markers for anti-cancer agents. The CC CC gene information for diagnosing prognosis is related to factors similar to that for N-myc and TrkA genes.

xx SQ Sequence 896 BP; 340 A; 169 C; 162 G; 216 T; 9 other;

Query Match 32.28; Score 790.2; DB 22; Length 896;  
Best Local Similarity 96.88; Pred. No. 5.3e-156;  
Matches 834; Conservative 0; Mismatches 25; Indels 3; Gaps 3;

Qy 542 TCGAATGCTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTAAAGG 601  
Db 17 TGGCCTACTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTAAAGG 76

Qy 602 ACTCAGTCTACTTTATGGTGTGATCTTGAACAACAAGCTACGAGATTCACCCAAA 661  
77 ACTCAGTCTACTTTATGGTGTGATCTTGAACAACAAGCTACGAGATTCACCCAAA 136

Qy 662 AGCCTTTCTAACCAACAAGAGTGGCAAGGCTGTATCTGTCCACAAATCAACTAAGTGA 721  
Db 137 AGCCTTTCTAACCAACAAGAGTGGCAAGGCTGTATCTGTCCACAAATCAACTAAGTGA 196

Qy 722 AATACCACTTAATCTTCCAAATCATTTAGCAGAACTCAGAAATCATGAAATAAAGTTAA 781  
Db 197 AATACCACTTAATCTTCCAAATCATTTAGCAGAACTCAGAAATCATGAAATAAAGTTAA 256

Qy 782 GAAATFACAAAGACACATTCAAAGAAATGAATGCTTTTACACGTTTGGAAATGAGTGC 841  
Db 257 GAAATFACAAAGACACATTCAAAGAAATGAATGCTTTTACACGTTTGGAAATGAGTGC 316

Qy 842 AAACCCCTCTTGATAATATGATGATAGAGGAGGAGGCTTTGAAGGGGTGAGGTTTCCA 901  
Db 317 AAACCCCTCTTGATAATATGATGATAGAGGAGGAGGCTTTGAAGGGGTGAGGTTTCCA 376

Qy 902 TATCAGAAATTCGAGAACAACCTGACCTCAGTTCTTAAAGGCTTACCACCACTTTATT 961  
Db 377 TATCAGAAATTCGAGAACAACCTGACCTCAGTTCTTAAAGGCTTACCACCACTTTATT 436

Qy 962 GGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGATA 1021  
Db 437 GGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGATA 496

Qy 1022 CAAGAAGTACAAAGGCTGGGCTTAGGAACAACAATAATCAGATATCGAAATGGAG 1081  
497 CAAGAAGTACAAAGGCTGGGCTTAGGAACAACAATAATCAGATATCGAAATGGAG 556

Qy 1082 TCTGTCTAACATACACGCTGTGAG - AGAAATACATTTTGGAAACAATAAATAAATAA 1140  
Db 557 TCTGTCTAACATACACGCTGTGAGAGAAATACATTTTGGGAACAATAAATAAATAA 616

Qy 1141 TCCCTTCAGGATACC - AGAGTTGAAATACCTCC - AGATAATCTTCCTTCATCTAATTC 1198  
Db 617 TCCCTTCAGGATACCAGAGTTGAAATACCTTCAAGATAATCTCCTTCATCTCAATTC 676

Qy 1199 AATTCGAAGAGTGGAGTAAATGATCTTCTCCACAGTCCCAAGATGAGAAATCTTT 1258  
Db 677 AATTCGAAGAGTGGAGTAAATGATCTTCTCCACAGTCCCAAGATGAGAAATCTTT 736

Qy 1259 ATACAGTGCATAGTTTATTTCAACACCGGCTGAAATCTTGGGAAATGCAACCTGCAAC 1318  
Db 737 ATACAGTGCATAGTTTATTTCAACACCGGCTGAAATCTTGGGAAATGCAACCTGCAAC 796

Qy 1319 ATTTCTGTTGTTTGTGAGCAGATAGTGTTCAGCTTTGGGAACCTTTGGAATGTAATAATT 1378  
Db 797 ATTTCTGTTGTTTGTGAGCAGATAGTGTTCAGCTTTGGGAACCTTTGGAATGTAATAATT 856

Qy 1379 AGTAATGGTAATGTCATTTA 1400

Db 857 AATAATGGCAATGTCANTTA 878

RESULT 14  
AAI61293  
ID AAI61293 standard; cDNA; 814 BP.  
XX AAI61293;  
XX AAI61293;  
XX 22-OCT-2001 (first entry)  
XX Human polynucleotide SEQ ID NO 5282.  
XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.  
XX Homo sapiens.  
OS WO200153312-A1.  
PN 26-JUL-2001.  
PD 26-DEC-2000; 2000WO-US34263.  
XX 21-JAN-2000; 2000US-0488725.  
PR 25-APR-2000; 2000US-0552317.  
PR 09-JUL-2000; 2000US-0598042.  
PR 19-JUL-2000; 2000US-0620312.  
PR 03-AUG-2000; 2000US-0653450.  
PR 14-SEP-2000; 2000US-0662191.  
PR 19-OCT-2000; 2000US-0693036.  
PR 29-NOV-2000; 2000US-0727344.  
XX (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;  
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
XX WPI; 2001-442253/47.  
DR P-PSDB; AAM42137.  
XX Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -  
PT Claim 1; SEQ ID NO 5282; 10078pp; English.  
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders.  
CC Note: The sequence data for this patent did not form part of the printed CC specification.  
XX  
SQ Sequence: 814 BP; 263 A; 166 C; 143 G; 242 T; 0 other;  
Query Match 32.08; Score 785.6; DB 22; Length 814;  
Best Local Similarity 98.88; Pred. No. 4.7e-155;



[illegible]



Db 241 TCGATGATGATGATGAGCAACTCTCTTTTCCACAAGAGAGCCAAAGAGCCATTTTTT 300  
QY 431 TCCATTTGATCTGTTCCCAATGTGCCATTTGGATGTCAGTCCTATTACGAGTTGTACA 490  
Db 301 TCCATTTGATCTGTTTCCCAATGTGCCATTTGGATGTCAGTCCTATTACGAGTTGTACA 360  
QY 491 TTGCTCAGATTTAGGTTTTCAGCTCAGTCCCAACCAACATTCCTATTGATCTCGAATGCT 550  
Db 361 TTGCTCAGATTTAGGTTTTCAGCTCAGTCCCAACCAACATTCCTATTGATCTCGAATGCT 420  
QY 551 TGATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGGACTCACTTC 610  
Db 421 TGATCTTCCAAAACAATAAATAAAGAAATCAAGAAATGATTTTAAAGGACTCACTTC 480  
QY 611 ACTTTATGTCGTGATCCTGAAACAACAAGCTAAGGAAATTCACCCAAAAGCCCTTCT 670  
Db 481 ACTTTATGTCGTGATCCTGAAACAACAAGCTAAGGAAATTCACCCAAAAGCCCTTCT 540  
QY 671 AACCCAAAAGAAGTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAATACCCT 730  
Db 541 AACCCAAAAGAAGTTGCGAAGGCTGTATCTGTCCCAACATCAACTAAGTGAATACCCT 600  
LW 731 TAATCTTCCAAAATCATTAGCAGAACTCAGAAATTCATGAAAAATAAGTTAAGAAAAATACA 790  
601 TAATCTTCCAAAATCATTAGCAGAACTCAGAAATTCATGAAAAATAAGTTAAGAAAAATACA 660  
QY 791 AAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAAACCTCT 850  
Db 661 AAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTGCAAAACCTCT 720  
QY 851 TGATAATAATGGGATAGACCCAGGGGCATTTGAAGGGGTGACGGTGTCCATATCAGAAT 910  
Db 721 TGATAATAATGGGATAGACCCAGGGGCATTTGAAGGGGTGACGGTGTCCATATCAGAAT 780  
QY 911 TGCAGAAGCAAAACTGACCTCAGTTCTTAAAGGCTTTACCCACCAACTTTAT 960  
Db 781 TGCAGAAGCAAAACTGAGNCTCAGTTCTTAAAGATATCTTCCTTCATTCT 830

Search completed: May 31, 2003, 10:54:25  
Job time : 563 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 10:30:17 ; Search time 3450 Seconds

(without alignments)  
11519.920 Million cell updates/sec

Title: US-09-944-884-1

Perfect score: 2454

Sequence: 1 ggactaatctggggagcag.....taaaaattgtttgaaat 2454

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

arched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*

1: em.estba:\*

2: em.esthum:\*

3: em.estin:\*

4: em.estmu:\*

5: em.estov:\*

6: em.estpl:\*

7: em.estro:\*

8: em.htc:\*

9: gb.est1:\*

10: gb.est2:\*

11: gb.htc:\*

12: gb.est3:\*

13: gb.est4:\*

14: gb.est5:\*

15: em.estfun:\*

16: em.estom:\*

17: gb.gss:\*

18: em.gss.hum:\*

19: em.gss.inv:\*

20: em.gss.pln:\*

21: em.gss.vrt:\*

22: em.gss.fun:\*

23: em.gss.mam:\*

24: em.gss.mus:\*

25: em.gss.other:\*

26: em.gss.pro:\*

27: em.gss.rod:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1134.8	46.2	2302	11 AK014504	AK014504 Mus muscu
C 2	665.8	27.1	695	14 BQ004507	BQ004507 UT-H-E10-
C 3	656.4	26.7	672	14 BM992531	BM992531 UT-H-DT0-
4	612.4	25.0	695	10 AW608047	AW608047 RC3-LT002
C 5	608	24.8	626	14 BQ574173	BQ574173 UT-H-E21-
6	587.8	24.0	592	9 AL600795	AL600795 DKEZp313E

7	585.2	23.8	926	14 BQ960688	BQ960688 AGENCOURT
8	579.6	23.6	632	10 AW961537	AW961537 EST373609
C 9	555	22.6	568	10 AW450923	AW450923 UT-H-BI3-
C 10	553.4	22.6	560	12 BF056897	BF056897 7K11G05.X
11	553	22.5	553	9 AL598934	AL598934 DKEZp313F
12	550.4	22.4	591	10 AW955638	AW955638 EST367708
13	527.4	21.5	529	9 AL135736	AL135736 DKEZp3860
C 14	522.4	21.3	533	10 AW192703	AW192703 x150a04.X
C 15	520.4	21.2	603	11 BC022059	BC022059 Homo sapi
C 16	512	20.9	517	12 BF056951	BF056951 7K12G05.X
C 17	511	20.8	517	9 AI655462	AI655462 tt13a07.X
C 18	505.4	20.6	510	10 AW337165	AW337165 xw81906.X
C 19	502.4	20.5	522	13 BM666200	BM666200 UT-E-DX1-
C 20	496	20.2	501	10 AW193820	AW193820 xm30f10.X
C 21	493	20.1	525	9 AI741321	AI741321 w920c02.X
C 22	486.6	19.8	641	10 BE374603	BE374603 60125391
C 23	482.4	19.7	497	10 AW338706	AW338706 ha64d03.X
C 24	477.4	19.5	482	12 BF108809	BF108809 7164d06.X
C 25	473.4	19.3	492	9 AL135737	AL135737 DKEZp3860
C 26	473	19.3	480	9 AI657039	AI657039 tt49d03.X
C 27	472.8	19.3	488	9 AI088424	AI088424 qbl17b10.X
C 28	471	19.2	473	9 AI493987	AI493987 q257e03.X
C 29	470.2	19.2	571	12 BG564080	BG564080 602586130
C 30	470	19.2	471	9 AI862037	AI862037 tw71a05.X
C 31	468	19.1	468	9 AI240315	AI240315 q114c02.X
C 32	467	19.0	491	10 BE049606	BE049606 xw91b10.X
C 33	465.4	19.0	477	9 AI148466	AI148466 qc39e12.X
C 34	464.8	18.9	469	10 AW237808	AW237808 xm81d12.X
C 35	462	18.8	496	9 AI539334	AI539334 te45g09.X
C 36	451.4	18.4	459	9 AI370866	AI370866 ta63h10.X
C 37	450.2	18.3	485	9 AI373846	AI373846 qz96a11.X
C 38	449.8	18.3	462	9 AI277357	AI277357 qm54b03.X
C 39	431.8	17.6	568	9 AI006670	AI006670 ue16b10.Y
C 40	424.4	17.3	476	12 BF823520	BF823520 MRI-RF003
C 41	424	17.3	429	10 AW002412	AW002412 wu61f07.X
C 42	422	17.2	480	9 AA330080	AA330080 EST33760
C 43	418	17.0	559	10 BE633222	BE633222 uv74d03.Y
C 44	415.4	16.9	418	14 N67239	N67239 yz48h02.s1
C 45	412.2	16.8	480	12 BF823517	BF823517 MRI-RF003

#### ALIGNMENTS

##### RESULT 1

AK014504

LOCUS

DEFINITION

Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4631401G09:asporin, full insert sequence.

ACCESSION

AK014504.1 GI:12852406

VERSION

HTC; CAP trapper.

KEYWORDS

Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA,

clone.lib:RIKEN full-length enriched mouse cDNA library

SOURCE

clone:4631401G09.

ORGANISM

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1

Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

PUBLISHED

99279253

10349636

REFERENCE

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

PUBLISHED

11042159

REFERENCE

3

**AUTHORS**  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

**TITLE**  
Riken integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

**JOURNAL**  
Genome Res. 10(11), 1757-1771 (2000)

MEDLINE PUBMED REFERENCE AUTHORS	
20530913 11076861 4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Konno, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Aono, H., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyooka, K., Wang, K. H., Weitz, C., Whittaker, C., Willming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Havashizaki, Y.

**TITLE** Functional annotation of a full-length mouse cDNA collection  
**JOURNAL** Nature 409 (6821), 685-690 (2001)

21085660  
11217851  
5 (bases 1 to 2302)  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,  
Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C.,  
Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T.,  
Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F.,  
Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S.,  
Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K.,  
Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J.,  
Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D.,  
Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F.,  
Tanaka, T., Tejlina, Y., Toyota, T., Yamamura, T., Yamahata, I.,  
Yasunishi, A., Yoshida, K., Yoshino, M., Murematsu, M. and  
Hayashizaki, Y.

**TITLE** Direct Submission  
**JOURNAL** Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-resesg@riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

document

```

with BamHI and XhoI. cDNA of size comprised longer than 7 kb was
selected before cloning. Vector: a modified pBluescript KS(+) after
bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3',
end: BamHI. Host: DH10B.

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         /tissue_type="Skin"
         /clone_lib="RIKEN full-length enriched mouse cDNA library"
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DB	73	GGTAGGAGGGCTGGATTTTGTCTCTTTTCTTTTCTTTTAAATGTAACACTTCTTTA	132	
QY	105	TCTTTTCTTCTTACACAGTCTGTGAGAACTTTACATTATAGATATAGTAGTACATGGTGG	164	
DB	133	TTTTTTTCTTCTTGAAGAGTCT-TGAGGATACTTACATTGCAGTTAAAGTAGTACAGGGTGG	191	
QY	165	ATAACTTCTACTTTTAGGAGGACTCTCTCTGACAGTCTTAGACTGGTCTTCTACAC	224	
DB	192	ATAAATCTACTTTGAAGAAACTCTCTCTCTGACAGTTGGACTTGTACAC-----	246	
QY	225	TAAACACCATGAAGGAGTATGTGCTCTATTATTCCTGGCTTTGTGCTCTGCCAAACCC	284	
DB	247	-AGGCCAGCATGAAGGAGTATGTGATGCTACTGCTTTTGGCTGTGCTCTGCCAAACCC	305	
QY	285	TTCTTTTAGCCCTTCACATCGCACTGAGAATATATGCTGTAAGGATATGGAAGACACA	344	
DB	306	TTCTTTTAGCCCTTCCACACACGACTGAGAATATATGATTTGAAGATATGGAAGACACA	365	
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648 ACAGATTTTCAACCAAAAGCCCTTTTCAACCAACAAGAGTTGGGAGGCTGTATTTATCC 707  
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## RESULT 2

B0004507/C

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

695 bp mRNA linear EST 26-MAR-2002  
UI-H-E10-ayo-c-13-0-UI.s1 NCI-CCAP\_E10 Homo sapiens cDNA clone  
IMAGE:5841348 3', mRNA sequence.

B0004507  
B0004507  
B0004507.1 GI:19729407  
EST.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 695)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 JOURNAL Tumor Gene Index  
 COMMENT Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: rcgaps-femail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES

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 Db 155 AACGACAGATCAATTAACACAGACAGAACCCGAAAGCTCTATATAAATGCTCAGAGTTC 96  
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 Db 95 TTTATGTAATTTCTTATTGGCATTCAACATATGTAAATCAGAAAAACAGGAAATTTTCA 36  
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BM992531 672 bp mRNA linear EST 17-JUN-2002  
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 IMAGE:5864192 3', mRNA sequence.

ACCESSION BM992531  
 VERSION BM992531.1 GI:19711920  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 672)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: rcgaps-femail.nih.gov  
 Tissue Procurement: Dr. Jose Mercuende  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

FEATURES

source	Location/Qualifiers
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	/lab_host="DH10B (Life Technologies)"
	/note="Organ: Lung; Vector: pT73-Pac (Pharmacia), with a modified polylinker; Site_1: Ecor I; Site_2: Not I; NCI_CGAP_DT0 is a cDNA library containing the following tissue(s): Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is AACTGTTCGG. TAG_LIB=UI-H-DT0 TAG_TISSUE=lung metastatic chondrosarcoma"

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Query Match      26.7%; Score 656.4; DB 14; Length 672;
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DB 612 TAATCATCTTAAAGATGATTTGATATAATCTTATTGAATTAACCTATCATGCTTTAGA 553
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DB 492 CAACCTTGATAATGCTTACTCATGAAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTT 433
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DB 432 TTTAATTTATACCTGATTTTAAATCTCTGTAAACAGCTGTAGTGTTCATATAAATCTGT 373
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DB 372 AACTGCGATTTTAATGATCGGTATTTAAGCTTTTAAAGCATGAAATTTGTTAGGCTA 313
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DB 312 TATAACATGTCACCTTCAACTCTAAGGAATATTTTGGATATATCCCTTTGGAGACCTTG 253
QY 2217 CTGGAAGAGCCTGGACACTAACAATTTACACAAATTTCTCTCAAAATAGTATGA 2276
DB 252 CTGGAAGAGCCTGGACACTAACAATTTACACAAATTTCTCTCAAAATAGTATGA 193
QY 2277 CTGGATACTCTGAGAAACACATCTAGTATTAAGTAAGTAAGCAAGCATCAAAATTAACA 2336
DB 192 CTGGATACTCTGAGAAACACATCTAGTATTAAGTAAGTAAGCAAGCATCAAAATTAACA 133
QY 2337 GACAGAAACCGAAAGCTCTATATAATGCTCAGAGTCTTTTATGATTTCTTTATGGCAT 2396
DB 132 GACAGAAACCGAAAGCTCTATATAATGCTCAGAGTCTTTTATGATTTCTTTATGGCAT 73
QY 2397 TCAACATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATTTGGTTGAAAT 2454
DB 72 TCAACATATGTAATAATCAGAAACAGGAAATTTTCATTAATAATATTTGGTTGAAAT 15

RESULT 4
LOCUS      AW608047
DEFINITION RC3-LT0023-200100-012-c10 LT0023 Homo sapiens cDNA, mRNA sequence.
ACCESSION  AW608047
VERSION     AW608047.1 GI:7312788
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 695)
AUTHORS   HCGP http://www.ludwig.org.br/ORESTES.
TITLE     The FAPESP/LICR Human Cancer Genome Project
JOURNAL   Unpublished (1999)
COMMENT   Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
```

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Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-LT0023-200100-012-c10&t3=2000-01-20&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence stop: 634.
Location/Qualifiers
    source          1..695
    /organism="Homo sapiens"
    /db_xref="taxon:9606"
    /clone_lib="LT0023"
    /dev_stage="Adult"
    /note="Organ: telomios; Vector: puc18; Site: SmaI;
    Site2: SmaI; A mini-library was made by cloning products
    derived from ORESTES PCR (U.S. Letters Patent application
    No. 196.716 - Ludwig Institute for Cancer Research)
    profiles into the puc 18 vector. Reverse transcription of
    tissue mRNA and cDNA amplification were performed under
    low stringency conditions."
    BASE COUNT      265 a      138 c      122 g      170 t
ORIGIN
Query Match      25.0%; Score 612.4; DB 10; Length 695;
Best Local Similarity 95.9%; Pred. No. 6.8e-108;
Matches 639; Conservative 0; Mismatches 26; Indels 1; Gaps 1;
QY 471 TGTATTACAGAGTTGTACATTTGCTCAGATTTAGTTTGGACCTCAGTCCCAACCAAT 530
DB 6 TGTATTACAGAGTTGTACATTTGCTCAGATTTAGTTTGGACCTCAGTCCCAACCAAT 65
QY 531 CCATTTGATCTCGAATGCTTGCATTTCAAAACAATAAATTAAGAAATCAAGAAAT 590
DB 66 CCATTTGATCTCGAATGCTTGCATTTCAAAACAATAAATTAAGAAATCAAGAAAT 125
QY 591 GATTTTAAAGGACTCACTTTCATTTATGCTGATCTGATCTGAACAACAACAGCTAAGCAAG 650
DB 126 GATTTTAAAGGACTCACTTTCATTTATGCTGATCTGATCTGAACAACAACAGCTAAGCAAG 185
QY 651 ATTCAACCCAAAAGCCCTTTCTTAACCAAAAAGAGTTTGCAGAGGCTGTATCTGTCCCAAT 710
DB 186 ATTCAACCCAAAAGCCCTTTCTTAACCAAAAAGAGTTTGCAGAGGCTGTATCTGTCCCAAT 245
QY 711 CAACTAAGTGAATACCACTTATCTTCCCAATCATATTAGCAGAACTCAGAAATTCATGAA 770
DB 246 CAACTAAGTGAATACCACTTATCTTCCCAATCATATTAGCAGAACTCAGAAATTCATGAA 305
QY 771 AATAAGTTAAGAAATACAAAAGGACACATTTCAAAGGAATGAATGCTTTACACGTTTGG 830
DB 306 AATAAGTTAAGAAATACAAAAGGACACATTTCAAAGGAATGAATGCTTTACACGTTTGG 365
QY 831 GAAATGAGTGAACCCCTCTTGATATAATGGATAGAGCCAGGGGCACTTTTGAAGGGTGG 890
DB 366 GAAATGAGTGAACCCCTCTTGATATAATGGATAGAGCCCTTGGGCACTTTTGAAGGGTGG 425
QY 891 ACGGTGTTCCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACCA 950
DB 426 ACGGTGTTCCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACCA 484
QY 951 CCAACTTTTATGGAGCTTTCACATTAGATTATATAATAATTTCAACAGTGAAGTTCAGGAT 1010
DB 485 CCAACTTTTATGGAGCTTTCACATTAGATTATATAATAATTTCAACAGTGAAGTTCAGGAT 544
QY 1011 TTTAAACGATACAAAGAACTACAAAGGCTGGCCCTAGGAAACAACAATACAGATATC 1070
DB 545 TTTAAACGATACAAAGAACTACAAAGGCTGGCCCTAGGAAACAACAATACAGATATC 604
QY 1071 GAAATGGGAGTCTTGCTAACATACACCTGTGAGAGAAATACATTTGGAAACATAATAA 1130
DB 605 GAAATGGGAGTCTTGCTAACATACACCTGTGAGAGAACTCATTTTGGAAACATAATAA 664
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QY      1131 CTRAAA 1136
Db      665 AAAAAA 670

RESULT 5
BO574173/c
LOCUS   BO574173      626 bp      mRNA      linear      EST 19-JUN-2002
DEFINITION   UI-H-EZ1-baz-i-13-0-UI.s1 NCI-CGAP_Ch2 Homo sapiens cDNA clone
              UI-H-EZ1-baz-i-13-0-UI 3', mRNA sequence.
ACCESSION   BO574173
VERSION     BO574173.1 GI:21477490
KEYWORDS    EST.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 626)
AUTHORS    NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE      National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
JOURNAL    Unpublished (1997)
COMMENT    Contact: Robert Strausberg, Ph.D.
            Email: cgaps-remail.nih.gov
            Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
            Orthopedics
            cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
            DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
            Clone Distribution: Clone distribution information can be obtained
            from Dr. M. Bento Soares, bento-soares@uiowa.edu
            The following repetitive elements were found in this cDNA
            sequence: 1-48, >AT-rich/low-complexity (matched complement)
            Seq.primer: M13 FORWARD
            POLYA=Yes.

FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="UI-H-EZ1-baz-i-13-0-UI"
                     /clone_lib="NCI-CGAP_Ch2"
                     /tissue_type="Chondrosarcoma Grade II"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Organ: Left Pelvis; Vector: p7T3-Pac (Pharmacia)
                     with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
                     NCI-CGAP_Ch2 is a normalized cDNA library containing the
                     following tissue(s): Chondrosarcoma Grade II. The library
                     was constructed according to Bonaldo, Lennon and Soares,
                     Genome Research, 6:791-806, 1996. First strand cDNA
                     synthesis was primed with an oligo-dr primer containing a
                     Not I site. Double stranded cDNA was ligated to an EcoR I
                     adaptor, digested with Not I, and cloned directionally
                     into p7T3-Pac vector. The oligonucleotide used to prime
                     the synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dr)18 tail. The sequence tag for this library is
                     TGATCACGCT.
     TAG_LIB=UI-H-EZ1
     TAG_TISSUE=grade-2-chondrosarcoma
     TAG_SEQ=ATCTAATATG"

BASE COUNT      215 a      87 c      95 g      229 t
ORIGIN

Query Match      24.8%; Score 608; DB 14; Length 626;
Best Local Similarity 100.0%; Pred. No. 4.9e-107;
Matches 608; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1847 GTAATATTTTAAATCATCTTAAAGTATGATGATATATATCTTATTGAAATACCTTATC 1906
Db      626 GTAATATTTTAAATCATCTTAAAGTATGATGATATATCTTATTGAAATACCTTATC 567

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/clone="DKFZp313E0538"
/clone_llb="J13 (synonym: hlcc2)"
/dev_stage="adult"
/lab_host="DH10B"
/note="Vector: pTriplex2; Site_1: SfiIA; Site_2: SfiIB;
      cDNA-collection"
BASE COUNT      180 a 124 c 110 g 178 t

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Query Match	24.0%	Score 587.8	DB 9	Length 592
Best Local Similarity	99.74	Pred. No. 3.8e-103		
Matches 589	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	115	TTACACAGTCTCTCAGAACATTTACATATAGATAAGTACATGCTGGATAACTTCTA	174	
Db	2	TTGACACAGTCTCGAGAACATTTACATATAGATAAGTACATGCTGGATAACTTCTA	61	
Db	175	CTTTTAGGAGGACTACTCTCTCTTGACAGTCCCTAGACTGGTCTTCTTACACTAAGACACCA	234	
Db	62	CTTTTAGGAGGACTACTCTCTCTTGACAGTCCCTAGACTGGTCTTCTTACACTAAGACACCA	121	
Qy	235	TGAAGGAGTATGTCCTCTATTTATTCCTGGCTTTGTGCTCTGCCAACCCCTTCTTTTAGCC	294	
Db	122	TGAAGGAGTATGTCCTCTATTTATTCCTGGCTTTGTGCTCTGCCAACCCCTTCTTTAGCC	181	
Qy	295	CTTCACACATCGCACTCAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATG	354	
Db	182	CTTCACACATCGCACTCAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATG	241	
Qy	355	ATGATGATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCCAACAGAGAGAC	414	
Db	242	ATGATGATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCCAACAGAGAGAC	301	
Qy	415	CAAGAAGCCATTTTTTTTCCATTTTCATCTGTTTCCAAATGTGCCAATTTGGATGTCACTGCT	474	
Db	302	CAAGAAGCCATTTTTTTTCCATTTTCATCTGTTTCCCAATGTGCCAATTTGGATGTCACTGCT	361	
Qy	475	ATTCACGAGTTGATACATTTGCTCAGATTTAGGCTTCAGCTCCAGTCCCAACCAACATTCAT	534	
Db	362	ATTCACGAGTTGATACATTTGCTCAGATTTAGGCTTCAGTCCCAACCAACATTCATTCAT	421	
Qy	535	TTGATCTCGAATGCTTGTATCTTCAAAACAATAAATTAAGGAATCAAGAAAATGATT	594	
Db	422	TTGATCTCGAATGCTTGTATCTTCAAAACAATAAATTAAGGAATCAAGAAAATGATT	481	
Db	595	TTAAAGGACTCACCTTCACTTTATGGTCTGATCTCTGAACAACAACAAGCTTAACGAAGATTC	654	
Db	482	TTAAAGGACTCACCTTCACTTTATGGTCTGATCTCTGAACAACAACAAGCTTAACGAAGATTC	541	
Qy	655	ACCCAAAGGCTTTTCTTAACCAACAAGATTTGCGAAGGCTGTATCTGTGCC	705	
Db	542	ACCCAAAGGCTTTTCTTAACCAACAAGATTTGCGAAGGCTGTATCTGTGCC	592	

RESULT 7	BO960688	926 bp	mRNA	linear	EST 21-AUG-2002
BO960688	ACGENCOURT_8840778	NIH_MGC_129	Mus musculus	cdna clone	IMAGE:6313764
LOCUS	5', mRNA sequence.				
DEFINITION	BO960688				
ACCESSION	BO960688				
VERSION	BO960688.1				
KEYWORDS	GI:22376166				
SOURCE	EST.				
ORGANISM	house mouse.				
	Mus musculus				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 926)				
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Susan L. Sullivan, PhD.				

CDNA Library Preparation: Resgen, Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
plate: LLNL13741 row: g column: 13  
High quality sequence stop: 710.

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1. <b>Feature 1</b>	Source 1
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3. <b>Feature 3</b>	Source 3
4. <b>Feature 4</b>	Source 4
5. <b>Feature 5</b>	Source 5
6. <b>Feature 6</b>	Source 6
7. <b>Feature 7</b>	Source 7
8. <b>Feature 8</b>	Source 8
9. <b>Feature 9</b>	Source 9
10. <b>Feature 10</b>	Source 10
11. <b>Feature 11</b>	Source 11
12. <b>Feature 12</b>	Source 12
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14. <b>Feature 14</b>	Source 14
15. <b>Feature 15</b>	Source 15
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98. <b>Feature 98</b>	Source 98
99. <b>Feature 99</b>	Source 99
100. <b>Feature 100</b>	Source 100

FEATURES	source
BASE COUNT	ORIGIN

Query Mat  
Best Loca  
Matches

Query Match	23.8%	Score 585.2;	DB 14;	Length 926;
Best Local Similarity	82.1%	Prod. No. 1.le-102;		
Matches	750;	Conservative	0;	Mismatches 120; Indels 44; Gaps 5;
Qy	72	TGTTTTTTCTCTTTAAATGTAATACCTCCCATCTTTCTCTTACACAGTGTCTGAGA	131	
Db	56	TTTTTTCCTCTCTTTAAATGTAACACTCTTTATTTTTCTCTCTGGAAGAGTCT-TGAGG	114	
Qy	132	ACATTTACATTTATAGATAAGTAGTACATGCTGGGATAACTTCTACTTTTAGAGAGCACTACT	191	
Db	115	ATACCTACATTCGAGTTAAAGTAGTACAGGGTGGATAAATCTACTTTGTAAGAAAACCTTCT	174	
Qy	192	CTCTTCTGACAGTCTCTAGACTGGTCTTCTACACTTAAGACACCATGAAGGAGTATGTGCTC	251	
Db	175	CTCCTCTGACA-----AGGCCACATGAAGGAGTATGTGATG	211	
Qy	252	CTATTTATTCCTTGGCTTTGTGCTCTGCCAAACCTTCTTTAGCCCTTCCACATCGCACTG	311	
Db	212	CTACTGCTTTTGGCTGTGTCTCTGCCAAACCTTCTTTAGCCCTTCCACACAGCACTG	271	
Qy	312	AAGAATATGATGCTGAAGGATATGGAACACACAGATGATGATGATGATGATGATGATGAT	371	
Db	272	AAGAAATATGATTTGAAGGATATGGAAGACACA-----GATGATGAC	313	
Qy	372	GATGATGATGATGAGGACAACTCTCTTTTCCACAAGAGAGCCAAAGGCCATTTTTTT	431	
Db	314	GATACGATGATGAGGACAACTCTCTTTTCCACGAAGAGCCAGTGAACCCCTTTTTTC	373	
Qy	432	CCATTTGATCTCTTTTCCAAATGTGCCAATTTGGATGTCTAGTGTCTATTCACGATTTGTACAT	491	
Db	374	CCTTTTCGATTTGTTTCCAAATGTGCCAATTTGGTGGTCCAAATGTTACTCTCGAGTTGTTTCAC	433	
Qy	492	TGCTCAGATTTAGTGTTCACCTCAGTCCCAACCAACATTCATTTGATACTCTCGAATGCTT	551	
Db	434	TGCTCTGATCTAGTGTCTGACATCGGTTCCAAACCAACATTCATTTGATCTCGAATGGTT	493	
Qy	552	GATCTTCAAAACAATAAATTAAGGAATTAAGAAATGATTTTAAGGAGTCACTTCA	611	
Db	494	GACCTTCAAAATAATAAATCAAGGAAATTAAGGAAATGACTTTAAGGAGTCACTTCA	553	
Qy	612	CTTTATGTCTGTCTCAACAACAACAGCTTAACGAAGATTCACCCAAAAGCCCTTTCTA	671	
Db	554	CTTTATGTCTGTCTGACACACACAAAGCTTAACGAAGTCAACAAAGTCACTTCTA	613	
Qy	672	ACCACAAAAGATTTGCGAAGCTGTATCTGTCCCAACATCAACTAAGTGAATACCACCT	731	
Db	614	ACCACAAAAGATTTGAGAAGGCTATATTTATCCCAACCAACATTAAGTGAATTTCCACTT	673	
Qy	732	AATCTTCCAAATCAATAGCAGAACTCAGAATTCATGAAAATAAAGTTTAAGAAAATACAA	791	



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Db 734 AAGGACAGCTTCAGGGAATGAATGCTTTACATGTTTTCGAAATGAGTGCACACCCCTCTT 793
QY 852 GATAATAATGGGATAGAGCCAGGGCATTGAAGGGTGACGGTGTTCATATACAAAT 911
Db 794 GAGAACACGGGATAGA-CCAGGGGCATTGAAGGGTGACAGTATTCATATCAGATC 852
QY 912 GCAGAGCAAAACTGACCTCAGCTTCTTAAAGGCTTACCACCACTTATTTGAGCTTCAC 971
Db 853 GCTGAGCAAAACTAACCTCTATCC-AAAGGGCTACCACCACTTGTGCTGAGCTTCAT 911
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Db 912 TTAGATTTTATAA 925

RESULT 8
LOCUS AW961537 632 bp mRNA linear EST 01-JUN-2000
DEFINITION EST373609 MAGE resequencences, MAGG Homo sapiens cDNA, mRNA sequence.
ACCESSION AW961537
VERSION AW961537.1 GI:8151221
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Hegde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt
I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, F.J. and
Quackenbush, J.
TITLE Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
JOURNAL Unpublished (2000)
COMMENT Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 160
Seq primer: Reverse.
FEATURES
Location/Qualifiers
1..632
/organism="Homo sapiens"
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/clone_lib="MAGE resequencences, MAGG"
/note="Vector: pBluescriptSkm"
COUNT 176 a 128 c 123 g 205 t
IN

Query Match 23.6%; Score 579.6; DB 10; Length 632;
Best Local Similarity 97.3%; Pred. No. 1.4e-101;
Matches 613; Conservative 0; Mismatches 9; Indels 8; Gaps 2;

QY 7 ATCTGTGGGAGCAGTTTATTCAGATATCACCCAGGGTGCAGGCACACACAGGAGTGTG 66
Db 1 ATCTGTGGGAGCAGTTTATTCAGATATCACCCAGGGTGCAGGCACACACAGGAGTGTG 60
QY 67 AAGGGTGTGTTTTCTTTTAAATGAATACCTCTCATCTTTTCTTTACACAGTGTG 126
Db 61 AAGGGTGTGTTTTCTTTTAAATGAATACCTCTCATCTTTTCTTTACACAGTGTG 120
QY 127 TCAGAACATTTACATATAGATAGTACATGTTGGTATCTTACTTTTAGGAGGA 186
Db 121 TCAGAACATTTACATATAGATAGTACATGTTGGTATCTTACTTTTAGGAGGA 180
QY 187 CTACTCTCTTCTGACAGTCTTACACTGGTCTTCTACACTAAAGACACCATGAGGAGTATG 246
Db 181 CTACTCTCTTCTGACAGTCTTACACTGGTCTTCTACACTAAAGACACCATGAGGAGTATG 240
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QY 247 TGTCTCTATTATTCCTGGCTTTGTGCTCTGCCAAACCCCTTCTTTAGCCCTTCACACATCG 306
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QY 307 CACTGAAGAATATGATGCTGAAGGATATGAAGACACA-----GATGATGATGATG 360
Db 301 CACTGAAGAATATGATGCTGAAGGATATGAAGACACAGATGATGATGATGATG 360
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 421 GCCATTTTTCATTTGATCTGTTTCCAAATGTCTTTCATTTGATGATGATGATGATGATGATG 480
Db 421 GCCATTTTTCATTTGATCTGTTTCCAAATGTCTTTCATTTGATGATGATGATGATGATGATG 480
QY 481 GAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTTGATA 540
Db 481 GAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCATTTGATA 540
QY 541 CTCGAATGCTTGTATCTTCAAAACAATAAAATTAAGGAAATCAACGAAATGATTTTAA 598
Db 541 CTCGAATGCTTGTATCTTCAAAACAATAAAATTAAGGAAATCAACGAAATGATTTTAA 600
QY 599 AGGACTCACTTCACTTTATGGTCTGATCCT 628
Db 601 GGGACTCACTTCACTTTATGGGCTGAACCT 630

RESULT 9
LOCUS AW450923/c 568 bp mRNA linear EST 17-FEB-2000
DEFINITION UI-H-BI3-all-f-02-0-UI.s1 NCI-CGAP_Sub5 Homo sapiens cDNA clone
IMAGE:2737275 3', mRNA sequence.
ACCESSION AW450923
VERSION AW450923.1 GI:6991699
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward
POLYA=Yes.
FEATURES
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NCI-CGAP_Sub5"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not 1; Site 2: Eco RI; NCI-CGAP_Sub5
is a subtracted library derived from NCI-CGAP_Sub4. The
NCI-CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI-CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI-CGAP_Kid3 pool 1 LLAM
3334-3337, 3682-3683, 3798-3803 (IMAGE Clonids
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1322376-1323911, 1456008-1456775, 1500552-1502855),  
NCI\_CGAP\_Kid5 pool 1 LLAM 3338-3342, 3722-3725, 3776-3778  
(IMAGE Clonoids 1323912-1325831, 1471368-1472903,  
1492104-1493255); NCI\_CGAP\_Lu5 pool 1 LLAM 3575-3582,  
3851-3854 (IMAGE Clonoids 1414920-1417991, 1520904-1522439  
); NCI\_CGAP\_GC4 pool 1 LLAM 3164-3167, 3716-3720,  
3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983,  
147552-1476743); NCI\_CGAP\_Pr22 pool 1 LLAM 2457-2459,  
2738-2759, 3062-3068 (IMAGE Clonoids 983608-986759  
1101192-1101959, 1217928-1220615); NCI\_CGAP\_Colo pool 1  
LLAM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255  
1144584-1145351). (10% of the driver population), plus a  
pool of 3,840 arrayed clones from NCI\_CGAP\_Sub1 (IMAGE  
Clonoids 2708616-2710535) and NCI\_CGAP\_Sub2 (IMAGE  
Clonoids 2710536-2712455) (10% of the driver population  
), plus a pool of 11,136 clones from NCI\_CGAP\_Sub3 (IMAGE  
Clonoids 2712456-2723591) (10% of the driver population),  
plus a pool of 5,472 clones from NCI\_CGAP\_Sub4 (IMAGE  
Clonoids 2723592-2728969) (70% of the driver population).  
Subtraction was performed as previously described (Bonald  
, Lennon & Soares (1996): Normalization and Subtraction:  
Two Approaches to Facilitate Gene Discovery. Genome  
Research 6, 791-806.  
TAG\_L1B-NCI\_CGAP\_Kid3  
TAG\_TISSUE-kidney  
TAG\_SEQ-AATGc"

BASE COUNT	190 a	82 c	92 g	204 t	ORIGIN
Query Match	22.6%	Score 555;	DB 10;	Length 568;	
Best Local Similarity	100.0%;	Pred. No. 7.8e-97;			
Matches 555;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Qy	1900	CCCTATCATGCTCTTAGAGCCGCTTTATATGTTTAAAACTAATTTCTTAAATAAAGCCTT	1959		
Db	568	CCCTATCATGCTCTTAGAGCCGCTTTATGTTTAAAACTAATTTCTTAAATAAAGCCTT	509		
Qy	1960	CAGTAAATGTTCAATACCAACTTCATAAATGCTACTCATAGAGCTGGTTGGGGCTATA	2019		
Db	508	CAGTAAATGTTCAATACCAACTTCATAAATGCTACTCATAGAGCTGGTTGGGGCTATA	449		
Qy	2020	GCATATGCTTTTTTTTTTTTAAATATTACCTGATTTAAAAATCTCTCTAAAAACGCTGAG	2079		
Db	448	GCATATGCTTTTTTTTTTTTAAATATTACCTGATTTAAAAATCTCTCTAAAAACGCTGAG	389		
Qy	2080	TGTTTTCATAAAATCTGTAACTCGCATTTTAAATGATCGCTATTATAAGCTTTTAAATAGCA	2139		
Db	388	TGTTTTCATAAAATCTGTAACTCGCATTTTAAATGATCGCTATTATAAGCTTTTAAATAGCA	329		
Qy	2140	TGAAATTTGTTAGGCTATATAAAGCTTCCCACTTCAACTCTAAGGAATATTTTTCAGATAT	2199		
Db	328	TGAAATTTGTTAGGCTATATAAAGCTTCCCACTTCAACTCTAAGGAATATTTTTCAGATAT	269		
Qy	2200	CCCTTTTGGAAAGACCTTGCTTTGGAAAGACCCCTGGACACTTAACAATTTCTACACCAAAATTCCT	2259		
Db	268	CCCTTTTGGAAAGACCTTGCTTTGGAAAGACCCCTGGACACTTAACAATTTCTACACCAAAATTCCT	209		
Qy	2260	CTTCAAAATACGTATGGACTGGATTAACCTCTCAGAAACACATCTAGTATAACTGAATAAGCA	2319		
Db	208	CTTCAAAATACGTATGGACTGGATTAACCTCTCAGAAACACATCTAGTATAACTGAATAAGCA	149		
Qy	2320	GAGCATCAAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTAT	2379		
Db	148	GAGCATCAAAATTAACAGACAGAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTAT	89		
Qy	2380	GTATTTTCTTATTTGGCATTTCAACATATATGTAATTCAGAAAAACAGGGAATTTTTCATTAANA	2439		
Db	88	GTATTTTCTTATTTGGCATTTCAACATATATGTAATTCAGAAAAACAGGGAATTTTTCATTAANA	29		
Qy	2440	ATATTGGTTTGAAT 2454			
Db	28	ATATTGGTTTGAAT 14			

RESULT 10	BF056897	560 bp	mRNA	linear	EST 16-OCT-2000
LOCUS	7k11d05.x1	NCI_CGAP_GC6	Homo sapiens	cdna	clone IMAGE:344128 3',
DEFINITION	mRNA sequence.				
ACCESSION	BF056897				
VERSION	BF056897.1	GI:10810793			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 560)				
JOURNAL	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .				
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:capbs-r@mail.nih.gov">capbs-r@mail.nih.gov</a> Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL, send email to: <a href="mailto:info@image.lnlni.gov">info@image.lnlni.gov</a> Seq primer: -400p from Gibco High quality sequence stop: 466. Location/Qualifiers 1- 560 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="IMAGE:344128" /clone_lib="NCI_CGAP_GC6" /tissue_type="pooled germ cell tumors" /lab_host="DH10B" /note="Vector: p7T7D-Pac (Pharmacia) with a modified polylinker; Site.1: Not I; Site.2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones from the same library (cloneIDs 1257096-1258631, 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. * BASE COUNT 190 a 81 c 92 g 197 t ORIGIN Query Match 22.68; Score 553.4; DB 12; Length 560; Best Local Similarity 99.8; Pred. No. 1.6e-96; Matches 554; Conservative 0; Mismatches 1; Indels 0; Gaps 0; Oy 1900 CCTTATCATGCTCTAGAGCCCGCTTTATGTTTAAAACTAATTTCTTTAAATAAAGCCTT 1959 Db 560 CCTTATCATGCTCTAGAGCCCGCTTTATGTTTAAAACTAATTTCTTTAAATAAAGCCTT 501 Oy 1960 CAGTAAATGTTCAATACCACACTTGATAAATGCTACTCATAGAGCTGGTTTGGGGCTATA 2019 Db 500 CAGTAAATGTTCAATACCACACTTGATAAATGCTACTCATAGAGCTGGTTTGGGGCTATA 441 Oy 2020 GCATATGCTTTTTTTTTTTTAAATTTATACCTGATTTAAAAATCTCTGTAAAAAGCTGTAG 2079 Db 440 GCATATGCTTTTTTTTTTTTAAATTTATACCTGATTTAAAAATCTCTGTAAAAAGCTGTAG 381 Oy 2080 TGTTTCATAAAATCTGTAACTCGCATTTTATATGATCCGCTATTATAAGCTTTTAAATAGCA 2139 Db 380 TGTTTCATAAAATCTGTAACTCGCATTTTATATGATCCGCTATTATAAGCTTTTAAATAGCA 321 Oy 2140 TGAAAATTTGTTAGGCTATATAACACTTCCCACTTCAAGCAATATTTTTCAGATAT 2199				



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Matches 579; Conservative 0; Mismatches 11; Indels 2; Gaps 2;
QY 1601 CGTACAATGATCTTACATAAAATCTCATGCTTGACCATTCCTCTTCTCATACAAAAAG 1660
Db 1 CGTACAATGATCTTACATAAAATCTCATGCTTGACCATTCCTCTTCTCATACAAAAAG 60
QY 1661 TAAGATATTCGGTATTTAAACACTTTGTTATCAAGCACATTTTAAAAAGAACTGTACTGTA 1720
Db 61 TAAGATATTCGGTATTTAAACACTTTGTTATCAAGCATATTTTAAAAAGAACTGTACTGTA 120
QY 1721 AATGAATGCTTGACTTAGCAAAATTTGCTCTTTCATTTCTGTAGAAAAAGAGAT 1780
Db 121 AATGAATGCTTGACTTAGCAAAATTTGCTCTTTCATTTCTGTAGAAAAAGAGAT 180
QY 1781 TAACAAGACACTAATGTAAGAGTGCATTAACACTATTTCTTTAGTAGTAACCTGGGT 1840
Db 181 TAACAAGACACTAATGTAAGAGTGCATTAACACTATTTCTTTAGTAGTAACCTGGGT 240
1841 AGTACTGTAATATTTTAAATCATCTTAAAGTATGATTTGATATAATCTTTATGAAATATAC 1900
Db 241 AGTACTGTAATATTTTAAATCATCTTAAAGTATGATTTGATATAATCTTTATGAAATATAC 300
QY 1901 CTTATCATGCTCTAGAGCCGCTTTATGTTTAAACACTAATTTCTTAAATAAAGCCCTTC 1960
Db 301 CTTATCATGCTCTAGAGCCGCTTTATGTTTAAACACTAATTTCTTAAATAAAGCCCTTC 360
QY 1961 AGTAATGTTCTATACCAACTTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAG 2020
Db 361 AGTAATGTTCTATACCAACTTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAG 420
QY 2021 CATATGCTTTTTTTTTTTTAAATTTATACCTGATTTTAAATAATCTCTGTAAAAACGTTAGT 2080
Db 421 CATATGCTTTTTTTTTTTTAAATTTATACCTGATTTTAAATAATCTCTGTAAAAACGTTAGT 479
QY 2081 GTTTCATAAAATCTGTAATCGCATTTTAAATGATCGCTATTATAGCTTTTAAATAG-CA 2139
Db 480 GTTTCATAAAATCTGTAATCGCATTTTAAATGATCGCTATTATAGCTTTTAAATAGCCT 539
QY 2140 TCAAAATCTTAGGCTATATACATTTGCCACTTCAACTCTAAGGAATATTTT 2191
Db 540 TCAAAATCTTAGGCTTTTAAACATTTGCCACTTCAACTTTTAAAGAAATTTT 591

RESULT 13
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NTION
529 bp mRNA linear EST 25-FEB-2000
DKFp58600417_r1 586 (synonym: hutel) Homo sapiens cDNA clone
AL135736
AL135736.1 GI:6603923
EST.
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 529)
AUTHORS
Koehler,K., Beyer,A., Mewes,H.W., Gassenhuber,J. and Wiemann,S.
TITLE
EST (Koehler, et al.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Koehler K
MIPS
Am Klopferspitz 18a D-82152 Martinsried, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMFZ (Biomedical Research Center at the Charite,
Berlin/Germany) within the cDNA sequencing consortium of the German
Genome Project.
SI sequence also available.
This clone (DKFp58600417) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.
Location/Qualifiers
FEATURES
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/dev_stage="adult"
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/note="Vector: pSport1; Site_1: NotI; Site_2: SalI/MluI"
BASE COUNT 179 a 88 c 76 g 186 t
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Best Local Similarity 99.8%; Pred. No. 1.6e-91;
Matches 528; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1859 ATCATCTTTAAAGTATGATTTGATATAATCTTATTGAAATACCTTATCATGCTCTAGAGC 1918
Db 1 ATCATCTTTAAAGTATGATTTGATATAATCTTATTGAAATACCTTATCATGCTCTAGAGC 60
QY 1919 CGGTCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCTTCAGTAAATGTTTCATTACCA 1978
Db 61 CGGTCTTTATGTTTAAAACTAATTTCTTAAAAATAAGCCTTCAGTAAATGTTTCATTACCA 120
QY 1979 ACTTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTT 2038
Db 121 ACTTGATAAATGCTACTCATAGAGCTGGTTGGGGCTATAGCATATGCTTTTTTTTTTTT 180
QY 2039 TAATTTATACCTGATTTTAAATATCTCTGTAATAAGCTGTAGTGTTCATAAATCTGTAA 2098
Db 181 TAATTTATACCTGATTTTAAATATCTCTGTAATAAGCTGTAGTGTTCATAAATCTGTAA 240
QY 2099 CTCGATTTTAAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAATGTTTAGGCTATA 2158
Db 241 CTCGATTTTAAATGATCGCTATTATTAAGCTTTTAAATAGCATGAAATGTTTAGGCTATA 300
QY 2159 TAACATTCGCACCTTCAACTCTAAGGAATATTTTGAAGATATCCCTTGGAGACCTTGCT 2218
Db 301 TAACATTCGCACCTTCAACTCTAAGGAATATTTTGAAGATATCCCTTGGAGACCTTGCT 360
QY 2219 TGAAGAGCTCGACACTAACAATTTCTACACAAATTTGCTCTTCAAAATACGTATGGACT 2278
Db 361 TGAAGAGCTCGACACTAACAATTTCTACACAAATTTGCTCTTCAAAATACGTATGGACT 420
QY 2279 GGATAACTCTGAGAACAACATCTAGTATAAATGAATAAGCAGCATCAAAATTAACACA 2338
Db 421 GGATAACTCTGAGAACAACATCTAGTATAAATGAATAAGCAGCATCAAAATTAACACA 480
QY 2339 CAGAAACCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATGTTTCT 2387
Db 481 CAGAAACCGAAAGCTCTATATAAAATGCTCAGAGTTCTTTTATGTTTCT 529

RESULT 14
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LOCUS
DEFINITION
x150a04.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2678094 3',
mRNA sequence.
ACCESSION
A1192703
VERSION
A1192703.1 GI:6471402
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 533)
AUTHORS
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Life Technologies catalog #: 11548-013
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DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
[www-bio.llnl.gov/bbrp/image/image.html](http://www-bio.llnl.gov/bbrp/image/image.html)  
 Seq primer: -40UP from Gibco  
 High quality sequence stop: 415.  
 Location/Qualifiers

## FEATURES

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 /clone\_lib="NCI CGAP Panel"  
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 /lab\_host="DH10B"  
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 Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dn.  
 Average insert size 1.72 kb. Life Technologies catalog #:  
 11548-013"

BASE COUNT 183 a 78 c 85 g 187 t

## ORIGIN

Query Match 21.3%; Score 522.4; DB 10; Length 533;  
 Best Local Similarity 99.8%; Pred. No. 1.5e-90;  
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 Oy 1931 TTAAGACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTCAATACCAACTTGATAAATG 1990  
 Db 525 TTTAAACTAATTTCTTAAATAAAGCCTTCAGTAAATGTTCAATACCAACTTGATAAATG 466  
 Oy 1991 CTACTCATAAGAGCTGCTTTGGGCTATAGCATATGCTTTTTTTTTTAAATATTACCT 2050  
 Db 465 CTACTCATAAGAGCTGCTTTGGGCTATAGCATATGCTTTTTTTTTTAAATATTACCT 406  
 Oy 2051 GATTAAAAATCTCTGTAAAAACGTGAGTGTTCATPAAATCTGTAACTCGCATTTTAA 2110  
 Db 405 GATTAAAAATCTCTGTAAAAACGTGAGTGTTCATPAAATCTGTAACTCGCATTTTAA 346  
 Oy 2111 TGATCCGCTATTATAAGCTTTTATAGCATGAAATTTGTTAGGCTATATACATATGCCAC 2170  
 Db 345 TGATCCGCTATTATAAGCTTTTATAGCATGAAATTTGTTAGGCTATATACATATGCCAC 286  
 Oy 2171 TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGAAGACCTTGCTTGAAGAGCCTG 2230  
 Db 285 TTCAACTCTAAGGAATATTTTGGAGATATCCCTTTTGAAGACCTTGCTTGAAGAGCCTG 226  
 Oy 2231 GACACTAACCAATTTCTACACCAAAATGTCCTTCAAAATACGTATGAGTGGATTAACCTGA 2290  
 Db 225 GACACTAACCAATTTCTACACCAAAATGTCCTTCAAAATACGTATGAGTGGATTAACCTGA 166  
 Oy 2291 GAAACACATCTAGTATACTGAATAAGCAGATCAAAATTAACAGACAGAAACCGAAA 2350  
 Db 165 GAAACACATCTAGTATACTGAATAAGCAGATCAAAATTAACAGACAGAAACCGAAA 106  
 Oy 2351 GCCTATATAAATGCTCAGAGTCTTTATCTATTTCTATTTGCGATTCACATATGTAAA 2410  
 Db 105 GCCTATATAAATGCTCAGAGTCTTTATGTATTTCTTATTTGGCATTCACATATGTAAA 46  
 Oy 2411 ATCAGAAAACAGGGAATTTTTCATTAATAAATATTTGGTTGAAAT 2454  
 Db 45 ATCAGAAAACAGGGAATTTTTCATTAATAAATATTTGGTTGAAAT 2

## RESULT 15

BC022059  
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 DEFINITION Homo sapiens, similar to asporin (LRR class 1), clone  
 IMAGE:4714902, mRNA.  
 ACCESSION BC022059  
 VERSION BC022059.1 GI:18314458  
 KEYWORDS HTC.  
 SOURCE Homo sapiens.  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

1 (bases 1 to 603)  
 Strausberg, R.  
 Direct Submission  
 Submitted (22-JAN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

## REMARK

COMMENT  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: CLONTECH  
 CDNA Library Preparation: CLONTECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: amadan@systemsbiology.org  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 38 Row: 0 Column: 2  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF  
 analysis, GenesScan gene prediction  
 This clone has the following problem: frame shifted.

## FEATURES

Location/Qualifiers  
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 /notes="Vector: pDNR-LJB"  
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## ORIGIN

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 Best Local Similarity 97.1%; Pred. No. 3.5e-90;  
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 Oy 1 GGACTAATCTGTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGCCACACGAGACT 60  
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 Oy 61 GTCTTGAAGGGTG-TTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTTTACA 119  
 Db 76 GTCTTGAAGGGTGTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTTTACA 135  
 Oy 120 CAGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATACTTCTACTTTT 179  
 Db 136 CAGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGGTGGATACTTCTACTTTT 195  
 Oy 180 AGGAGGACTACTCTCTTCTGACAGTCTTACAGTGGTCTTCTACACTAAGACACCATGAAG 239  
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 Oy 240 GAGTATGTCTCTCTATTTATCTGCTTCTGCTTGCCTGCTGCTGCTTCTTACCCCTTCA 299  
 Db 256 GAGTATGTCTCTCTATTTATTCCT-GCTTTGTCTCTGCCAAACCTTCTTTAGCCCTTCA 314  
 Oy 300 CACATCGCACTGAAGAATATGATGCTGAAGGATATGAAGACACACA---GATGATGATGAT 356  
 Db 315 CACATCGCACTGAAGAATATGATGCTGAAGGATATGAAGACACACAGATGATGATGATGAT 374  
 Oy 357 GAT 416  
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Db 495 TCACGAGTTGTACATTTGCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTTCCA-TT 553
Qy 537 GATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAATCAAAAGA 586
Db 554 GATACTCGAATGCTTGATCTTCAAAACAATAAAATTAAGGAATCAAAAGA 603
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Search completed: May 31, 2003, 13:38:00  
Job time : 3455 secs

GenCore version 5:1.6  
Copyright (c) 1993 - 2003 Compuquen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 31, 2003, 10:41:47 ; Search time 343 Seconds  
(without alignments) 9646.904 Million cell updates/sec

**Title:** US-09-944-884-1  
**Perfect score:** 2454  
**Sequence:** 1 ggactaatctgtggagcag.....taaaaaatatggtttgaaat 2454

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

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searched:      845702 seqs, 674182571 residues
Total number of hits satisfying chosen parameters: 1691404

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 s

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- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/ptodata/1/pubpna/US09\_PUBCOMB.seq.\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			ID	Description
	Score	Match	Length		
1	2454	100.0	2454	9	US-09-944-413-1
2	2454	100.0	2454	9	US-09-944-403-1
3	2454	100.0	2454	9	US-09-944-896-1
4	2454	100.0	2454	9	US-09-944-904-1
5	2454	100.0	2454	9	US-09-944-947-1
6	2454	100.0	2454	9	US-09-944-929-1
7	2454	100.0	2454	9	US-10-028-072-327
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## ALIGNMENTS

RESULT 1  
US-09-944-413-1  
; Sequence 1, Application US/09944413

Patent No. US20020156004A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin  
APPLICANT: Botstein, David  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gerritsen, Mary  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul  
APPLICANT: Grimaldi, Christopher  
APPLICANT: Gurney, Austin  
APPLICANT: Hillan, Kenneth  
APPLICANT: Kijavlin, Ivar  
APPLICANT: Napier, Mary  
APPLICANT: Roy, Margaret  
APPLICANT: Tomas, Daniel  
APPLICANT: Wood, William

APPLICANT: WOOG, WILLIAM  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

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; FILE REFERENCE: P2548PICI
; CURRENT APPLICATION NUMBER: IIS/09/944 413

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 ;  
 : CURRENT APPLICATION NUMBER: US/09/544,415  
 : CURRENT FILING DATE: 2001-09-26

; CURRENT FILING DATE: 2001-03-20  
 ; PRIOR APPLICATION NUMBER: 09/856,028

;; PRIOR FILING DATE: 2001-05-25  
;; PRIOR APPLICATION NUMBER: 09/800,020

PRIOR FILING DATE: 2001-03-23  
PRIOR APPLICATION NUMBER: 60/067,411

PRIOR FILING DATE: December 3, 1997

PRIOR APPLICATION NUMBER: 60/069,334

PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069335

PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,278

;  
PRIOR FILING DATE: December 11, 1997

; PRIOR APPLICATION NUMBER: 60/069,425

; PRIOR FILING DATE: December 12, 1997

• PRIOR APPLICATION NUMBER: 60/069,696

; PRIOR FILING DATE: December 16, 1997

; PRIOR APPLICATION NUMBER: 60/069,694

; PRIOR FILING DATE: December 16, 1997



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Query Match      100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2  
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; Sequence 1, Application US/09944403  
; Patent No. US20020165143A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548PICI  
; CURRENT APPLICATION NUMBER: US/09/944,403  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998  
; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998



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RESULT 3  
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: Sequence 1, Application US/09944896  
: Patent No. US20020168715A1  
: GENERAL INFORMATION:  
: APPLICANT: Baker, Kevin  
: APPLICANT: Botstein, David  
: APPLICANT: Eaton, Dan  
: APPLICANT: Ferrara, Napoleone  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Gerritsen, Mary  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul  
: APPLICANT: Grimaldi, Christopher  
: APPLICANT: Gurney, Austin  
: APPLICANT: Hillan, Kenneth  
: APPLICANT: Kiljavin, Ivar  
: APPLICANT: Napier, Mary  
: APPLICANT: Roy, Margaret  
: APPLICANT: Tumas, Daniel  
: APPLICANT: Wood, William  
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
: FILE REFERENCE: P2548P1C1  
: CURRENT APPLICATION NUMBER: US/09/944, 896  
: CURRENT FILING DATE: 2001-08-31  
: PRIOR APPLICATION NUMBER: 09/866, 028  
: PRIOR FILING DATE: 2001-05-25  
: PRIOR APPLICATION NUMBER: 60/069, 334  
: PRIOR FILING DATE: December 11, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 335  
: PRIOR FILING DATE: December 11, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 278  
: PRIOR FILING DATE: December 11, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 425  
: PRIOR FILING DATE: December 12, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 696  
: PRIOR FILING DATE: December 16, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 694  
: PRIOR FILING DATE: December 16, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 702  
: PRIOR FILING DATE: December 16, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 870  
: PRIOR FILING DATE: December 17, 1997  
: PRIOR APPLICATION NUMBER: 60/069, 873  
: PRIOR FILING DATE: December 17, 1997  
: PRIOR APPLICATION NUMBER: 60/068, 017  
: PRIOR FILING DATE: December 18, 1997  
: PRIOR APPLICATION NUMBER: 60/070, 440  
: PRIOR FILING DATE: January 5, 1998  
: PRIOR APPLICATION NUMBER: 60/074, 086  
: PRIOR FILING DATE: February 9, 1998  
: PRIOR APPLICATION NUMBER: 60/074, 092  
: PRIOR FILING DATE: February 9, 1998  
: PRIOR APPLICATION NUMBER: 60/075, 945  
: PRIOR FILING DATE: February 25, 1998  
: PRIOR APPLICATION NUMBER: 60/112, 850  
: PRIOR FILING DATE: December 16, 1998  
: PRIOR APPLICATION NUMBER: 60/113, 296  
: PRIOR FILING DATE: December 22, 1998  
: PRIOR APPLICATION NUMBER: 60/146, 222  
: PRIOR FILING DATE: July 28, 1999  
: PRIOR APPLICATION NUMBER: PCT/US98/19330  
: PRIOR FILING DATE: September 16, 1998  
: PRIOR APPLICATION NUMBER: PCT/US98/25108  
: PRIOR FILING DATE: December 1, 1998  
: PRIOR APPLICATION NUMBER: 09/216, 021  
: PRIOR FILING DATE: December 16, 1998  
: PRIOR APPLICATION NUMBER: 09/218, 517  
: PRIOR FILING DATE: December 22, 1998

;; PRIOR APPLICATION NUMBER: 09/254,311  
;; PRIOR FILING DATE: March 3, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: September 15, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28409  
;; PRIOR FILING DATE: No. US20020168715Aember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. US20020168715Aember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
;; PRIOR FILING DATE: December 1, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: December 16, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: March 2, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: March 30, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: May 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/20710  
;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520  
;; PRIOR FILING DATE: February 28, 2001  
;; NUMBER OF SEQ ID NOS: 120  
;; SEQ ID NO 1  
;; LENGTH: 2454  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-09-944-896-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 601 GACTCAGTCTTATGCTGATCTGAACAACAACAAGCTAACGAAGATTCACCCAA 660  
DB 601 GACTCAGTCTTATGCTGATCTGAACAACAACAAGCTAACGAAGATTCACCCAA 660

QY 661 AAGCCTTTTCAACCAACAAGAAGTTGCAAGGCTGTATCTGTCCCAACAATAAAGT 720  
DB 661 AAGCCTTTTCAACCAACAAGAAGTTGCAAGGCTGTATCTGTCCCAACAATAAAGT 720

QY 721 AAATACCACTTAATCTTTCCCAAAATCATTTAGCAGAACTCAGAAATTCATGAAATTAAGTTA 780  
DB 721 AAATACCACTTAATCTTTCCCAAAATCATTTAGCAGAACTCAGAAATTCATGAAATTAAGTTA 780

QY 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACAGCTTTTGGAAATGAGTG 840  
DB 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACAGCTTTTGGAAATGAGTG 840

QY 841 CAAACCTCTTTGATAATAAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900  
DB 841 CAAACCTCTTTGATAATAAATGGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTTC 900

QY 901 ATATCAGATTGCAAGAACAAAACCTGACCTCAGTCTTCTTAAAGGCTTACCACCACTTTAT 960  
DB 901 ATATCAGATTGCAAGAACAAAACCTGACCTCAGTCTTCTTAAAGGCTTACCACCACTTTAT 960

QY 961 TGGAGCTTCTAGATTATAAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020  
DB 961 TGGAGCTTCTAGATTATAAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020

QY 1021 ACRAAGAACTACRAAGCTGGGCTAGGAACACAAATACAGATATCGAAATGGA 1080  
DB 1021 ACRAAGAACTACRAAGCTGGGCTAGGAACACAAATACAGATATCGAAATGGA 1080

QY 1081 GTCTTGCTACATACACCGTGTGAGAAATACATTTTGGAAACAAATAAATAAATAA 1140  
DB 1081 GTCTTGCTACATACACCGTGTGAGAAATACATTTTGGAAACAAATAAATAAATAA 1140

QY 1141 TCCCTTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCAATTTCAATCAA 1200  
DB 1141 TCCCTTCAGGATTTACCAGAGTTGAAATACCTCCAGATAATCTTCTTCAATTTCAATCAA 1200

QY 1201 TTGCAAGAGTGGGAGTAAATCACCTTCTCCACAGTCCCAAGATGAAGAAATCTTTAT 1260  
DB 1201 TTGCAAGAGTGGGAGTAAATCACCTTCTCCACAGTCCCAAGATGAAGAAATCTTTAT 1260

QY 1261 ACAGTCAATTAAGTTTATTCACAAACCCGGTGAATATCTGGGAATGCAACCTGCAACAT 1320  
DB 1261 ACAGTCAATTAAGTTTATTCACAAACCCGGTGAATATCTGGGAATGCAACCTGCAACAT 1320

QY 1321 TTGCTTGTGTTTGGAGCAGATGATGCTCAGCTTTGGAACTTTGGAAATGTAATAATTAG 1380  
DB 1321 TTGCTTGTGTTTGGAGCAGATGATGCTCAGCTTTGGAACTTTGGAAATGTAATAATTAG 1380

QY 1381 TAATGCTAATGCTCAATTTAATAAGATTCAAAATCCCTACATTTGGAAATGCTTCAAC 1440  
DB 1381 TAATGCTAATGCTCAATTTAATAAGATTCAAAATCCCTACATTTGGAAATGCTTCAAC 1440

QY 1441 TCTATTAAATAGTGTAGTATTATATACAGCAAAATATCTTCTCAAGTGGTGAAGTCC 1500  
DB 1441 TCTATTAAATAGTGTAGTATTATATACAGCAAAATATCTTCTCAAGTGGTGAAGTCC 1500

QY 1501 ACTGACTTTATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAACTATTGATACATAAG 1560  
DB 1501 ACTGACTTTATTTATGACAAAGAAATTTCAACGGAAATTTGCCAAACTATTGATACATAAG 1560

QY 1561 GGGTTGAGAGAAACAAGCATCTATTGCGATTTCTTTTTCGGTACAAATGATCTTACATA 1620

[illegible]

## RESULT 4

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US-091-944-944-1
: Sequence 1, Application US/09944944
: Patent No. US20020173463A1
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerlitsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul

```





1801 AGAGTGCAATACATATCTTCTTTAGTAACCTGGGTAGTACTGTATATTTTAT 1860  
1801 AGAGTGCAATACATATCTTCTTTAGTAACCTGGGTAGTACTGTATATTTTAT 1860  
1861 CATCTAAAGTATGATTTGATATATCTTATTGAATACCTTATCATGCTTAGAGCC 1920  
1861 CATCTAAAGTATGATTTGATATATCTTATTGAATACCTTATCATGCTTAGAGCC 1920  
1921 GTCTTATCTTTAAACAACTATTTCTTTAAATTAAGCTTCTAGTAATGTTCAATACCAAC 1980  
1921 GTCTTATCTTTAAACAACTATTTCTTTAAATTAAGCTTCTAGTAATGTTCAATACCAAC 1980  
1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTT 2040  
1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTT 2040  
2041 ATATATACCTGATTTAAAAATCTGTAAAAACGCTGTAGTGTTCATAAATCTGTAAT 2100  
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2101 CGCATTTTAAATGATCGCTTATTAAGCTTTTAAATAGCATGAAATTTGTAGGCTATATA 2160  
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2221 GAAGACCTGGACACTAACAATTTCTACACCAATTTCTCAATAGATGTTGTTGAAATCTGACTGG 2280  
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2281 ATAACTCTGAGAAACACATCTAGTATACTGAATAGCAGAGCATCAAAATTAACACAGACA 2340  
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2401 CATATGTAATCAGAAACAGGGAATTTTCAATTTGAAAT 2454

RESULT 5  
US-09-944-907-1  
; Sequence 1, Application US/09944907  
; Publication No. US20020198147A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; CURRENT APPLICATION NUMBER: US/09/944, 907  
; CURRENT FILING DATE: 2001-08-31  
; PRIOR APPLICATION NUMBER: 09/866, 028

; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 1  
; LENGTH: 2454  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-907-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAAATCTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGGCACACCAAGGACT 60  
Db 1 GGACTAAATCTGGGAGCAGTTTATCCAGTATACCCAGGGTGCAGGCACACCAAGGACT 60  
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Db 61 GTGTTGAAGGGTGTCTTTCTTTAAATGAATACCTCCTCACTCTTCTTCTTACAC 120  
QY 121 AGTGCTCTGAGAACATTTACATTATAGTAAGTAGTACATGGTGGATACTTCTACTTTTA 180  
Db 121 AGTGCTCTGAGAACATTTACATTATAGTAAGTAGTACATGGTGGATACTTCTACTTTTA 180  
QY 181 GGAGGACTACTCTCTTCTGACAGTCTGAGTGGTCTTCTACACTAAGACACCATGAAGG 240  
Db 181 GGAGGACTACTCTCTTCTGACAGTCTGAGTGGTCTTCTACACTAAGACACCATGAAGG 240  
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QY 301 ACATGCACTGAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360  
Db 301 ACATGCACTGAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360  
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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Db 481 GAGTTGATGCTCAGATTTAGGTTTTCACCTCAGTCCCAACCAACATTTCCATTTGATA 540  
QY 541 CTCGAATGCTGATCTTCAAAACATATAAATTAAGGAAATCAAGAAATGATTTTAAAG 600  
Db 541 CTCGAATGCTGATCTTCAAAACATATAAATTAAGGAAATCAAGAAATGATTTTAAAG 600  
QY 601 GACTCACTTCACTTTATGCTGCTGATCTCAACAAACAAAGCTTAACGAGATTCACCCAA 660  
Db 601 GACTCACTTCACTTTATGCTGCTGATCTCAACAAACAAAGCTTAACGAGATTCACCCAA 660  
QY 661 AAGCCCTTCTAACCAACAAAGAGTTCGGAAGGCTGTATCTGTCGCCACATCAACTAAGTG 720  
Db 661 AAGCCCTTCTAACCAACAAAGAGTTCGGAAGGCTGTATCTGTCGCCACATCAACTAAGTG 720  
QY 721 AAATACCACTTAACTTCTCCAAATCATTAGCAGAACTCAGAATTCATGAAAATAAAGTTA 780  
Db 721 AAATACCACTTAACTTCTCCAAATCATTAGCAGAACTCAGAATTCATGAAAATAAAGTTA 780  
QY 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACACGTTTTTGGAAATGAGTG 840  
Db 781 AGAAATACAAAGGACACATTTCAAGGAATGAATGCTTTTACACGTTTTTGGAAATGAGTG 840  
QY 841 CAAACCCCTCTGATATAATGAGTATGAGCCAGGGCAATTTGAAGGGGTGACGGTCTCC 900  
Db 841 CAAACCCCTCTGATATAATGAGTATGAGCCAGGGCAATTTGAAGGGGTGACGGTCTCC 900  
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Db 901 ATATCAGAAATGCGAGAGCAAAAGTACCTCAGTCTCTTAAAGGCTTACCACCACTTTAT 960  
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Db 961 TGGAGCTTCACCTTAGATATATAATAAATTTCAACAGTGGAACTTTGAGGATTTTAAACGAT 1020  
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Db 1021 ACAAAGAACTTACAAAGGCTGGGCTAGGAAACAACAATAATCACAGATATCGAAATGGGA 1080  
QY 1081 GTCTTGCTAACATACCACGCTGTGAGAAATACATTTTGGAAACAATAAATAAATAA 1140  
Db 1081 GTCTTGCTAACATACCACGCTGTGAGAAATACATTTTGGAAACAATAAATAAATAA 1140  
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Db 1201 TTGCAAGAGTGGGAGTAATGACTTCTGTCCAACAGTGGCAAGAGATGAAGAAATCTTTAT 1260  
QY 1261 ACAGTCCAATAAGTTTATTCACCAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320  
Db 1261 ACAGTCCAATAAGTTTATTCACCAACCCGGTGAATACTGGGAAATGCAACCTGCAACAT 1320  
QY 1321 TTGCTTGTGTTTGGAGCAGAAATGAGTTCAGCTTGGGAACCTTGGAAATGTAATAATTAG 1380  
Db 1321 TTGCTTGTGTTTGGAGCAGAAATGAGTTCAGCTTGGGAACCTTGGAAATGTAATAATTAG 1380  
QY 1381 TAATGCTAATGCTTAAATATAGATTCAAAATCCCTACATTTGGAAATCTTGAAC 1440  
Db 1381 TAATGCTAATGCTTAAATATAGATTCAAAATCCCTACATTTGGAAATCTTGAAC 1440  
QY 1441 TCTAATTAATGCTAGTATTATATACAAAGCAAAATATCTATCTCAAGTGTAAAGTCC 1500  
Db 1441 TCTAATTAATGCTAGTATTATATACAAAGCAAAATATCTATCTCAAGTGTAAAGTCC 1500  
QY 1501 ACTGACTTATTTATGACAAGAAATTTCAACGGAATTTTGGCAAACTATTGATACATAAG 1560  
Db 1501 ACTGACTTATTTATGACAAGAAATTTCAACGGAATTTTGGCAAACTATTGATACATAAG 1560  
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Db 1561 GGGTTGAGAGAAACAAGCATCTATTCAGTTCCTTTTGGCGTACAAATGATCTTACATA 1620  
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Db 1621 AATCTCATGCTTGACCATTCCTTTTCTTCAACAAAAGTAAAGATATTCGGTATTAAAC 1680  
QY 1681 ACTTTGTTATCAAGCACATTTTAAAGAACTACTGTAAATGGAATGCTTGACATTAGC 1740  
Db 1681 ACTTTGTTATCAAGCACATTTTAAAGAACTACTGTAAATGGAATGCTTGACATTAGC 1740  
QY 1741 AAAAAATTTGCTCTTTCATTTCTGTTAGAAAAACAAGATTTTAAAGAACTAAATGTTGA 1800  
Db 1741 AAAAAATTTGCTCTTTCATTTCTGTTAGAAAAACAAGATTTTAAAGAACTAAATGTTGA 1800  
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Db 1801 AGAGTGCATACACTATCTTATCTTTAGTAACTTGGGTAGTACTGTAATATTTTAAAT 1860  
QY 1861 CATCTTAAAGTATGATTTGATATAATCTTATGAAATACCTTATCATGCTTTAGAGCCC 1920  
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATGAAATACCTTATCATGCTTTAGAGCCC 1920  
QY 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAAGCTTTCAGTAAATGTTTATCAACCAAC 1980  
Db 1921 GTCTTTATGTTTAAACTAATTTCTTAAATAAAGCTTTCAGTAAATGTTTATCAACCAAC 1980  
QY 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTA 2040

Db 1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTT 2040  
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Db 2041 ATTATTTACCTGATTTTAAATAATCTCTGTAAAAACGTGTAGTGTTCATAAAATCTGTAAC 2100  
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Db 2101 CGCATTTTAAATGATCGCTTATTATAGCTTTTAAATAGCATGAAATTTGTTAGCTATATA 2160  
QY 2161 ACATTTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGTCTTG 2220  
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Db 2221 GAAGACCTTGGACACTTAACAATTTACACCAATTTGTCTCTCAATAGCTATGAGACTGG 2280  
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QY 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTTCTTTATGTATTTCTTATTTGCGATTCAA 2400  
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QY 2401 CATATGTAATAATCAGAAACAGGGAAATTTTCAATTAATAATATTTGGTTTGAAT 2454  
Db 2401 CATATGTAATAATCAGAAACAGGGAAATTTTCAATTAATAATATTTGGTTTGAAT 2454

## RESULT 6

US-09-944-929-1

; Sequence 1, Application US/09944929

; Publication No. US20020197612A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Gerlitsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul

; APPLICANT: Grimaldi, Christopher

; APPLICANT: Gurney, Austin

; APPLICANT: Hillan, Kenneth

; APPLICANT: Kljavin, Ivar

; APPLICANT: Napier, Mary

; APPLICANT: Roy, Margaret

; APPLICANT: Tumas, Daniel

; APPLICANT: Wood, William

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P2548P1C1

; CURRENT APPLICATION NUMBER: US/09/944, 929

; CURRENT FILING DATE: 2001-08-31

; PRIOR APPLICATION NUMBER: 09/866, 028

; NUMBER OF SEQ ID NOS: 120

; SEQ ID NO: 1

; LENGTH: 2454

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-944-929-1

Query Match 100.0%; Score 2454; DB 9; Length 2454;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAATCTGTGGGAGCAGTTTATTCAGTATCCAGGCTGCGACACACAGGACT 60

Db 1 GGACTAATCTGTGGGAGCAGTTTATTCAGTATCCAGGCTGCGACACACAGGACT 60

QY 61 GTGTTGAAGGGTGTGTTTTTCTTTTAAATGAATACCTCCCATCTTTTCTTTTACAC 120  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GTGTTGAAGGGTGTGTTTTTCTTTTAAATGAATACCTCCCATCTTTTCTTTACAC 120  
QY 121 AGTGCTGAGAACATTTACATTAATAGATAGATAGATAGATAGATAGATAGATAGAT 180  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 AGTGCTGAGAACATTTACATTAATAGATAGATAGATAGATAGATAGATAGATAGAT 180  
QY 181 GGAGGACTACTCTCTCTGACAGTCTCTAGACGGTCTCTACACTAAGACACACATGAAG 240  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 GGAGGACTACTCTCTCTGACAGTCTCTAGACGGTCTCTACACTAAGACACACATGAAG 240  
QY 241 AGTATGTCTCTATTATTTCTGGCTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 AGTATGTCTCTATTATTTCTGGCTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
QY 301 ACATCGCACTGAAGAAATATGATGCTGAAGATATGAAGACACAGATGATGATGATG 360  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 ACATCGCACTGAAGAAATATGATGCTGAAGATATGAAGACACAGATGATGATGATG 360  
QY 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420  
QY 421 GCCATTTTTCATTTGATCTGTTTCCAAATGTCATTTGGATGTCAGTGTCTATTTCAC 480  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
421 GCCATTTTTCATTTGATCTGTTTCCAAATGTCATTTGGATGTCAGTGTCTATTTCAC 480  
QY 481 GAGTTGTACATTTGCTCAGATTTAGTTTGAACCTCAGTCCCAACACATTCATTTGATA 540  
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481 GAGTTGTACATTTGCTCAGATTTAGTTTGAACCTCAGTCCCAACACATTCATTTGATA 540  
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601 GACTCAGTTTCACTTTATGCTGCTGATCCTGAACAACAAGCTTAACGAAGATTCACCCAA 660  
QY 661 AAGCCTTTCTAACCAACAAGAGTTCGAAGGCTGTATCTGCTCCCAACAATCAACTAAGTG 720  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
661 AAGCCTTTCTAACCAACAAGAGTTCGAAGGCTGTATCTGCTCCCAACAATCAACTAAGTG 720  
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721 AAATACCACTTAATCTTCCCAATCATATAGCAGACTCAGATTCATGAATAAAGTTA 780  
QY 781 AGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTG 840  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
781 AGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAAATGAGTG 840  
QY 841 CAAACCTCTTGATTAATATGGAATAGACCCAGGGGATTTGAAGGGGTGACGGTGTCC 900  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
841 CAAACCTCTTGATTAATATGGAATAGACCCAGGGGATTTGAAGGGGTGACGGTGTCC 900  
QY 901 ATATCAGAAATTCAGAGCAAACTGACCTCAGTTTCCCTAAGGCTTTACCAACCACTTTAT 960  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
901 ATATCAGAAATTCAGAGCAAACTGACCTCAGTTTCCCTAAGGCTTTACCAACCACTTTAT 960  
QY 961 TGGAGCTTCACATTAATATAAATTTCAACAGTGAAGCTTGAAGGATTTTAAACGAT 1020  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
961 TGGAGCTTCACATTAATATAAATTTCAACAGTGAAGCTTGAAGGATTTTAAACGAT 1020  
QY 1021 ACAAGAAGACTCAAAAGGCTGGGCTAGGAACAACAATAATCAGATATCGAAATGGGA 1080  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1021 ACAAGAAGACTCAAAAGGCTGGGCTAGGAACAACAATAATCAGATATCGAAATGGGA 1080  
QY 1081 GTCCTGCTTAACATACACCTGTGAGAGAAATACATTTGGAAACAATAAATAAATAA 1140  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1081 GTCCTGCTTAACATACACCTGTGAGAGAAATACATTTGGAAACAATAAATAAATAA 1140

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DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1141 TCCCTTCAGGATTAACAGAGTTGAAATACCTCCAGATAAATCTTCTCATTTCAATCAA 1200  
QY 1201 TTGCAAGAGTGGAGTAATGACTTCTGTCACACAGTGCACAAAGATGAAGAATCTTTAT 1260  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1201 TTGCAAGAGTGGAGTAATGACTTCTGTCACACAGTGCACAAAGATGAAGAATCTTTAT 1260  
QY 1261 ACAGTGCATAAGTTTATTTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACAT 1320  
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1261 ACAGTGCATAAGTTTATTTCAACAACCCGGTGAAATACTGGGAAATGCAACCTGCAACAT 1320  
QY 1321 TTGCTGTGTTTGGAGCAGAAATGAGTGTTCAGTGTGGGAACCTTGAATGTAATATAG 1380  
DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1321 TTGCTGTGTTTGGAGCAGAAATGAGTGTTCAGTGTGGGAACCTTGAATGTAATATAG 1380  
QY 1381 TAAATGGTAATGCTCCATTTAATATAGATTCACAAATCCCTACATTTGGAATACATGAC 1440  
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1441 TCTATTAAATAGTGTATTTATATATACAAACAATATCTTCTCAAGTGTGAAGTCC 1500  
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1861 CATCTTAAAGTATGATTTGATATAATCTTATTTGAAATTAACCTTATCATCTTTAGAGCCC 1920  
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RESULT 7

US-10-028-072-327  
; Sequence 327, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
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? PRIOR FILING DATE: 1998-07-07

Query Match      100.0%; Score 2454; DB 9; Length 2454;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 181 GGAGGACTACTCTCTCTGACAGTCTTCTACACTGGTCTTCTACACTAAGACACCATCAAGG 240
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Db 361 ATGATGATGATGATGATGATGATGAGGACAACTCTCTTTTCCAAACAGAGAGCCCAAGAA 420
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Db 421 GCCATTTTCTCCATTTGATCTCTTTCCAAATGTGCTCATTTGGATGCTAGTGTATTTCAC 480
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Db 1921 GTCCTTATGTTTAAACTAATTTCTTAAATAAAGCCTTCAGTAATGTTTCATATACCAAC 1980  
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## RESULT 8

US-10-121-049-327  
; Sequence 327, Application US/10121049  
; Publication No. US2003002239A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C17  
; CURRENT APPLICATION NUMBER: US/10/121.049  
; CURRENT FILING DATE: 2002-04-12  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 327  
; LENGTH: 2454  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-121-049-327

Query Match 100.0%; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGACTAATCTGTGGAGCAGTCTTTTCCAGTATACCCAGGGTGCAGCCACACAGGACT 60  
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QY 61 GTGTTGAAGGGTGTCTTTTCTTTTAAATGTAATACCTCTCATCTTTTCTTTCTTACAC 120  
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Db 1801 AGAGTGCATACACTATTCTTATCTTTAGTAAGTGGGTAGTACTGTAATATTTTAAAT 1860  
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## RESULT 11

US-10-175-746-327  
; Sequence 327, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin

;; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
;; FILE OF INVENTION: ACIDS ENCODING THE SAME  
;; CURRENT APPLICATION NUMBER: P3330R1C353  
;; CURRENT FILING DATE: 2002-06-19  
;; Prior Application removed - See File Wrapper or Palm  
;; NUMBER OF SEQ ID NOS: 550  
;; SEQ ID NO 327  
;; LENGTH: 2454  
;; TYPE: DNA  
;; ORGANISM: Homo Sapien  
US-10-175-746-327

Query Match 100.0%; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1921 GTCTTTATGTTTAAACCTAATTTCTTAAATTAAGCCCTTCAGTAATGTTCAATTAACCAAC 1980
Qy 1981 TTGATAAATGCTACTATAAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTATA 2040
Db 1981 TTGATAAATGCTACTATAAGAGCTGTTTGGGGCTATAGCATATGCTTTTCTTTTATA 2040
Qy 2041 ATATTACCTGATTTAAATAATCTCTGTAATAACGTTAGTCTTTTCAATAAAATCTGTAAC 2100
Db 2041 ATATTACCTGATTTAAATAATCTCTGTAATAACGTTAGTCTTTTCAATAAAATCTGTAAC 2100
Qy 2101 CGCAATTTAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
Db 2101 CGCAATTTAATGATCCGCTATTATAAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160
Qy 2161 ACATTGCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGGCTTG 2220
Db 2161 ACATTGCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTGGCTTG 2220
Qy 2221 GAAGAGCCTGGACACTAACAATTTACACCAAAATTTGCTCTTCAAAATACGTATGCACTGG 2280
Db 2221 GAAGAGCCTGGACACTAACAATTTACACCAAAATTTGCTCTTCAAAATACGTATGCACTGG 2280
Qy 2281 ATAACTCTGAGAACACATCTAGTATTAACCTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Db 2281 ATAACTCTGAGAACACATCTAGTATTAACCTGAATAAGCAGAGCATCAAAATTAACAGACA 2340
Qy 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGTTATTTCTTATTTGGCATTCAA 2400
Db 2341 GAAACCGAAAGCTCTATATAAATGCTCAGAGTCTTTATGTTATTTCTTATTTGGCATTCAA 2400
Qy 2401 CATATGTAATCAGAAAACAGGGAATTTTCAATAAAATATTTGGTTGAAAT 2454
Db 2401 CATATGTAATCAGAAAACAGGGAATTTTCAATAAAATATTTGGTTGAAAT 2454
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## RESULT 12

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US-10-176-918-327
; Sequence 327, Application US/10176918
; Publication No. US200300275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC382
; CURRENT FILING DATE: 2002-06-20
; NUMBER OF SEQ ID NOS: 550
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-327
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Query Match 100.08; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.08; Pred. No. 0;

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Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGACTAATCTGTGGAGCAGTTTATTCAGTATATCACCAGGTGAGCCACACAGGACT 60
Db 1 GGACTAATCTGTGGAGCAGTTTATTCAGTATATCACCAGGTGAGCCACACAGGACT 60
Qy 61 GTGTTGAAGGCTGTTTTTCTTTTAAATGTAATACCTCTCATCTCTTCTTTTACAC 120
Db 61 GTGTTGAAGGCTGTTTTTCTTTTAAATGTAATACCTCTCATCTCTTCTTTTACAC 120
Qy 121 AGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGTGGATACTTCTACTTTTA 180
Db 121 AGTGTCTGAGAACATTTACATTATAGATAAGTAGTACATGTGGATACTTCTACTTTTA 180
Qy 181 GGAGSACTACTCTCTCTGACAGTCTTAGACTGCTTCTACACTTAAGACACCATGAAG 240
Db 181 GGAGSACTACTCTCTCTGACAGTCTTAGACTGCTTCTACACTTAAGACACCATGAAG 240
Qy 241 AGTATGTCTCTTATTTCTGACAGTCTTAGACTGCTTCTGCAAAACCTTCTTTAGCCCTTCAC 300
Db 241 AGTATGTCTCTTATTTCTGACAGTCTTAGACTGCTTCTGCAAAACCTTCTTTAGCCCTTCAC 300
Qy 301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360
Db 301 ACATCGCACTGAAGAATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360
Qy 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
Qy 421 GCCATTTTCTTCCATTTGATCTGTTCCAAATGCTGCTTCCAAATGCTGCTTCCAAATGCTGCT 480
Db 421 GCCATTTTCTTCCATTTGATCTGTTCCAAATGCTGCTTCCAAATGCTGCTTCCAAATGCTGCT 480
Qy 481 GAGTTGTACATGCTCAGATTTAGTTTGCCTCAGTCCCAACCAACATTCATTTTGATA 540
Db 481 GAGTTGTACATGCTCAGATTTAGTTTGCCTCAGTCCCAACCAACATTCATTTTGATA 540
Qy 541 CTGCAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTTAAAG 600
Db 541 CTGCAATGCTTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGATTTTAAAG 600
Qy 601 GACTCACTTCACTTTATGCTGCTGATCCTGAAACAACAACAGCTTAACGAAGATTCACCCAA 660
Db 601 GACTCACTTCACTTTATGCTGCTGATCCTGAAACAACAACAGCTTAACGAAGATTCACCCAA 660
Qy 661 AAGCCTTTCTAACCAACAAGAGCTTGCAGAGGCTGTATCTGCTCCCAACATCAACTAAGTG 720
Db 661 AAGCCTTTCTAACCAACAAGAGCTTGCAGAGGCTGTATCTGCTCCCAACATCAACTAAGTG 720
Qy 721 AAATACACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAATAAAGTTA 780
Db 721 AAATACACTTAATCTTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAATAAAGTTA 780
Qy 781 AGAAATACAAAGGACACATTCAAAGGATGAATGCTTTTACAGTTTGGAAATGAGTG 840
Db 781 AGAAATACAAAGGACACATTCAAAGGATGAATGCTTTTACAGTTTGGAAATGAGTG 840
Qy 841 CAAACCTCTTGATAATAATGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTCC 900
Db 841 CAAACCTCTTGATAATAATGGATAGAGCCAGGGCATTTGAAGGGGTGACGGTGTCC 900
Qy 901 ATATCAGAATTCAGAAAGCAAACTGACCTCAGTTCTTAAAGGCTTTACCACCACTTTAT 960
Db 901 ATATCAGAATTCAGAAAGCAAACTGACCTCAGTTCTTAAAGGCTTTACCACCACTTTAT 960
Qy 961 TGSAGCTTCACTTAGATTTATAAATAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020
Db 961 TGSAGCTTCACTTAGATTTATAAATAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020
Qy 1021 ACAGAGAACTACAAAGGCTGGGCTAGGAAACCAACAAATACAGATATCGGAAATGGA 1080
Db 1021 ACAGAGAACTACAAAGGCTGGGCTAGGAAACCAACAAATACAGATATCGGAAATGGA 1080
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1081 GTCTTCTTAACATACACGCTGTGAGAGAAATACATTGGGAAACAATAAATAAATAA 1140  
Db GTCTTCTTAACATACACGCTGTGAGAGAAATACATTGGGAAACAATAAATAAATAA 1140  
1141 TCCCTTCAGGATACAGAGTGAATACCTCCAGATAATCTTCCCTTCATTCTTAATTCAA 1200  
Db TCCCTTCAGGATACAGAGTGAATACCTCCAGATAATCTTCCCTTCATTCTTAATTCAA 1200  
1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGGCCAAAGATGAAGAAATCTTTAT 1260  
Db TTGCAAGAGTGGGAGTAAATGACTTCTGTCCAAACAGTGGCCAAAGATGAAGAAATCTTTAT 1260  
1261 ACAGTGCATAAGTTTATTCACAAACCCGCTGAAATCTAGTGGGAAATGCAACCTGCAACAT 1320  
Db ACAGTGCATAAGTTTATTCACAAACCCGCTGAAATCTAGTGGGAAATGCAACCTGCAACAT 1320  
1321 TTGCTTGTCTTTGACGAGAAATGCTGCTGAGCTTGGGAACTTTGGAATGTAATAATTAG 1380  
Db TTGCTTGTCTTTGACGAGAAATGCTGCTGAGCTTGGGAACTTTGGAATGTAATAATTAG 1380  
1381 TAATTGGTAAATGCCATTTAATAAGATTCAAATAATCCCTACATTTGGAAATCTTTGAAC 1440  
Db TAATTGGTAAATGCCATTTAATAAGATTCAAATAATCCCTACATTTGGAAATCTTTGAAC 1440  
1441 TCTATTAAATAGGTAGTATTATATATACAAAGCAAAATATCTATCTCAAGTGGTAAAGTCC 1500  
Db TCTATTAAATAGGTAGTATTATATATACAAAGCAAAATATCTATCTCAAGTGGTAAAGTCC 1500  
1501 ACTGACTTATTTATCACAGAAATTTACAGGAAATTTGCCAAACTATTGATACATAAG 1560  
Db ACTGACTTATTTATCACAGAAATTTACAGGAAATTTGCCAAACTATTGATACATAAG 1560  
1561 GGGTTGAGAGAAACAAGCATCTATTGCAGTTTCTCTTTTGGCTACAAATGATCTTACATA 1620  
Db GGGTTGAGAGAAACAAGCATCTATTGCAGTTTCTCTTTTGGCTACAAATGATCTTACATA 1620  
1621 AATCTCATGCTTGACCATTCCTTTCTTTCATACAAAGAAAGTAAAGATTCGGTATTTAAC 1680  
Db AATCTCATGCTTGACCATTCCTTTCTTTCATACAAAGAAAGTAAAGATTCGGTATTTAAC 1680  
1681 ACTTTGCTATCAAGACATTTTAAAGAACTACTGTAAATGGAAATGCTTCACTTAC 1740  
Db ACTTTGCTATCAAGACATTTTAAAGAACTACTGTAAATGGAAATGCTTCACTTAC 1740  
1741 AAAAAATGCTCTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAAGTGA 1800  
Db AAAAAATGCTCTTTCATTTGCTGTAGAAAAACAGAAATTAACAAAGACAGTAAGTGA 1800  
1801 AGAGTGCATTACACTATCTTATCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860  
Db AGAGTGCATTACACTATCTTATCTTTAGTAACTTTGGGTAGTACTGTAATATTTTAAAT 1860  
1861 CATCTTAAAGTATGATTGATATAATCTTATTTGAAATACCTTATCATGCTTTAGAGCC 1920  
Db CATCTTAAAGTATGATTGATATAATCTTATTTGAAATACCTTATCATGCTTTAGAGCC 1920  
1921 GTCCTTATGTTTAAACTAATTTCTTAAATAAGCTTCAGTAAATGTTTCATTACCAAC 1980  
Db GTCCTTATGTTTAAACTAATTTCTTAAATAAGCTTCAGTAAATGTTTCATTACCAAC 1980  
1981 TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTTA 2040  
Db TTGATAAATGCTACTCATAGAGCTGGTTTGGGCTATAGCATATGCTTTTTTTTTTTTA 2040  
2041 ATTATTACCTGATTTAAATCTCTCTAATAAGCTGTAGTGGTTTCATAAATCTGTAAT 2100  
Db ATTATTACCTGATTTAAATCTCTCTAATAAGCTGTAGTGGTTTCATAAATCTGTAAT 2100  
2101 CGCATTTTAAATGATCGCTATTATAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160  
Db CGCATTTTAAATGATCGCTATTATAGCTTTTAAATAGCATGAAATTTGTTAGGCTATATA 2160

2161 ACATTGCCACTTCAACTCTAAGGAATATTTTTCAGATATATCCCTTTGGAAGACCTTGGTTG 2220  
Db ACATTGCCACTTCAACTCTAAGGAATATTTTTCAGATATATCCCTTTGGAAGACCTTGGTTG 2220  
2221 GAAGACCTTGGACACTAACAATTTCTACACCAAAATTTGCTCTTCAAAATACGTTATGGACTGG 2280  
Db GAAGACCTTGGACACTAACAATTTCTACACCAAAATTTGCTCTTCAAAATACGTTATGGACTGG 2280  
2281 ATAACTCTTGAGAAACACATCTAGTATAAAGTGAATAAGCAGAGCATCAAAATTAACAGACA 2340  
Db ATAACTCTTGAGAAACACATCTAGTATAAAGTGAATAAGCAGAGCATCAAAATTAACAGACA 2340  
2341 GAAACGGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATATTTCTTATTTGGCATTCAA 2400  
Db GAAACGGAAGCTCTATATAAATGCTCAGAGTTCTTTATGATATTTCTTATTTGGCATTCAA 2400  
2401 CATATGTAATAATCAGAAAAACAGGAAATTTTTCATTAATAAATATTTGGTTTCAAAAT 2454  
Db CATATGTAATAATCAGAAAAACAGGAAATTTTTCATTAATAAATATTTGGTTTCAAAAT 2454

## RESULT 13

US-10-176-921-327

Sequence 327, Application US/10176921

Publication No. US20030027276A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.  
APPLICANT: Beresini, Maureen  
APPLICANT: DeForge, Laura  
APPLICANT: Desnoyers, Luc  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Sherwood, Steven  
APPLICANT: Smith, Victoria  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K  
APPLICANT: Wood, William  
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

FILE INVENTION: ACIDS ENCODING THE SAME

FILE REFERENCE: P3330R1C288

CURRENT APPLICATION NUMBER: US/10/176, 921

CURRENT FILING DATE: 2002-06-20

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 550

SEQ ID NO 327

LENGTH: 2454

TYPE: DNA

ORGANISM: Homo Sapien

US-10-176-921-327

Query Match 100.0%; Score 2454; DB 9; Length 2454;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACTAATCTGTGGAGCAGCTTTATTCACGATATCACCCAGGGTGCAGCCACACAGGACT 60  
Db 1 GGACTAATCTGTGGAGCAGCTTTATTCACGATATCACCCAGGGTGCAGCCACACAGGACT 60  
QY 61 GTGTTGAAGGCTGTTTTTTTCTTTTAAATGTAATACCTCTCTATCTTTCTTCTTACAC 120  
Db 61 GTGTTGAAGGCTGTTTTTTTCTTTTAAATGTAATACCTCTCTATCTTTCTTCTTACAC 120  
QY 121 AGTGTCTGAGAACATTTACATTTAGATAAGTAGTACATAGTGGATAAATCTTACTTTTA 180  
Db 121 AGTGTCTGAGAACATTTACATTTAGATAAGTAGTACATAGTGGATAAATCTTACTTTTA 180  
QY 181 GGAGGACTACTCTCTTCTGTACAGTCTAGAGTGGTCTTCTTACATAGACACCATGAAGG 240

|||||  
Db 181 GGAGGACTACTCTCTTCTGACAGCTCTAGACTGCTCTACACTAAGACACCATGAAGG 240  
Qy 241 AGTATGTGCTCCTATTATTCCTGGCTTGTGCTCTGCGCAACCCCTCTTTAGCCCTTCAC 300  
Db 241 AGTATGTGCTCCTATTATTCCTGGCTTGTGCTCTGCGCAACCCCTCTTTAGCCCTTCAC 300  
Qy 301 ACATCGGCACTGAAGNATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360  
Db 301 ACATCGGCACTGAAGNATATGATGCTGAAGGATATGGAAGACACAGATGATGATGATG 360  
Qy 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
Db 361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
Qy 421 GCCATTTTTTCCATTTGATGCTGTTTCCAAATGTGTCCTATTTGGATGTGCTATTCCAC 480  
Db 421 GCCATTTTTTCCATTTGATGCTGTTTCCAAATGTGTCCTATTTGGATGTGCTATTCCAC 480  
Qy 481 GAGTGTACATTTGCTCAGATTTAGGTTTGACTGACTGCTCCCAACCAACATTCATTTGATA 540  
Db 481 GAGTGTACATTTGCTCAGATTTAGGTTTGACTGACTGCTCCCAACCAACATTCATTTGATA 540  
Qy 541 CTCGAATGCTTGATCTTCAAAACAAATAAAATTAAGGAATCAAGAAAAATGATTTAAAG 600  
Db 541 CTCGAATGCTTGATCTTCAAAACAAATAAAATTAAGGAATCAAGAAAAATGATTTAAAG 600  
Qy 601 GACTCAGTCTACTTTATGCTGCTGATCTGCTGAACCAACCAACCAAGATTCACCCAA 660  
Db 601 GACTCAGTCTACTTTATGCTGCTGATCTGCTGAACCAACCAACCAAGATTCACCCAA 660  
Qy 661 AAGCCTTTCTAACCAACAAGATTTGCGAAGGCTGATCTGTCCCAACCAATCAACTAAGTG 720  
Db 661 AAGCCTTTCTAACCAACAAGATTTGCGAAGGCTGATCTGTCCCAACCAATCAACTAAGTG 720  
Qy 721 AAATACCACTTAATCTCCCAATCATTTAGCAGACTCAGAAATTCATCAAAATTAAGTTA 780  
Db 721 AAATACCACTTAATCTCCCAATCATTTAGCAGACTCAGAAATTCATCAAAATTAAGTTA 780  
Qy 781 AGAAATACAAAGGACACATTCRAAGGAATGAATGCTTTACACGTTTTGGAAATGAGTG 840  
Db 781 AGAAATACAAAGGACACATTCRAAGGAATGAATGCTTTACACGTTTTGGAAATGAGTG 840  
Qy 841 CAACCCCTCTTGATTAATGCGGATAGACCGAGGGCAATTTGAAGGGTGACGGTGTCC 900  
Db 841 CAACCCCTCTTGATTAATGCGGATAGACCGAGGGCAATTTGAAGGGTGACGGTGTCC 900  
Qy 901 ATATCAGAAATGCAGAGCAAAACTGACCTCAGTTTCTTAAAGGCTTACCACCACTTTAT 960  
Db 901 ATATCAGAAATGCAGAGCAAAACTGACCTCAGTTTCTTAAAGGCTTACCACCACTTTAT 960  
Qy 961 TGGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020  
Db 961 TGGAGCTTCACTTAGATTATATAAAATTTCAACAGTGGAACTTGAGGATTTTAAACGAT 1020  
Qy 1021 ACAAGAACTACAAGGCTGGGCTAGGAACACAAATACAGATATCGGAATGGGA 1080  
Db 1021 ACAAGAACTACAAGGCTGGGCTAGGAACACAAATACAGATATCGGAATGGGA 1080  
Qy 1081 GTCTTGCTTAACATACACGCTGTGAGAGAAATACATTTGGAAAAACAATAAATTAAGAAA 1140  
Db 1081 GTCTTGCTTAACATACACGCTGTGAGAGAAATACATTTGGAAAAACAATAAATTAAGAAA 1140  
Qy 1141 TCCCTTCAGGATACAGAGTTGAAATACCTCCAGATAATCTCTCTCATTTCAATTCAA 1200  
Db 1141 TCCCTTCAGGATACAGAGTTGAAATACCTCCAGATAATCTCTCTCATTTCAATTCAA 1200  
Qy 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCCAAAGATGAAGAAATCTTTAT 1260  
Db 1201 TTGCAAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCCAAAGATGAAGAAATCTTTAT 1260  
Qy 1261 ACAGTGCAATTAAGTTTATTAACAAACCCGGTGAATACTGGGAATGCAACCTGCAACAT 1320  
|||||

Db 1261 ACAGTGCAATTAAGTTTATTAACAAACCCGGTGAATACTGGGAATGCAACCTGCAACAT 1320  
Qy 1321 TTCGTTGTTGTTTTGAGCAGAATGAGTTTCAGCTTGGGAACCTTTGGAAATGAATAATTAG 1380  
Db 1321 TTCGTTGTTGTTTTGAGCAGAATGAGTTTCAGCTTGGGAACCTTTGGAAATGAATAATTAG 1380  
Qy 1381 TAAATGGTAAATGTCCTATTAATATAAGATTCAAAATCCCTACATTTGGAAATGCTGAAC 1440  
Db 1381 TAAATGGTAAATGTCCTATTAATATAAGATTCAAAATCCCTACATTTGGAAATGCTGAAC 1440  
Qy 1441 TCTATTAATAATAGGTAGTATTATATACAAAGCAAAATCTATTCTCAAGTGGTAAAGTCC 1500  
Db 1441 TCTATTAATAATAGGTAGTATTATATACAAAGCAAAATCTATTCTCAAGTGGTAAAGTCC 1500  
Qy 1501 ACTGACTTTATTTATGACAGAAAATTTCAACGGAAATTTTGCCAACTATTGATACATAAG 1560  
Db 1501 ACTGACTTTATTTATGACAGAAAATTTCAACGGAAATTTTGCCAACTATTGATACATAAG 1560  
Qy 1561 GGGTTGAGAGAAACAAGCATCTATTGCGATTTCCCTTTTGGGTACAAATGATCTACATA 1620  
Db 1561 GGGTTGAGAGAAACAAGCATCTATTGCGATTTCCCTTTTGGGTACAAATGATCTACATA 1620  
Qy 1621 AATCTCATGCTTGACCATTTCTTCTCATACAAAAGTAAGATATTCGGTATTTAAAC 1680  
Db 1621 AATCTCATGCTTGACCATTTCTTCTCATACAAAAGTAAGATATTCGGTATTTAAAC 1680  
Qy 1681 ACTTTGTTTATCAAGCACATTTTAAAGAACTGCTACTGTAATGAAATGCTTACTTACG 1740  
Db 1681 ACTTTGTTTATCAAGCACATTTTAAAGAACTGCTACTGTAATGAAATGCTTACTTACG 1740  
Qy 1741 AAAATTTGCTCTTTTCATTTGCTGTTAGAAAACAGAAATTAACAAGACAGTAAATGTA 1800  
Db 1741 AAAATTTGCTCTTTTCATTTGCTGTTAGAAAACAGAAATTAACAAGACAGTAAATGTA 1800  
Qy 1801 AGAGTGCAATTAACATTTCTTCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAAAT 1860  
Db 1801 AGAGTGCAATTAACATTTCTTCTTTAGTAACCTTGGGTAGTACTGTAATATTTTAAAT 1860  
Qy 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTTATCATGCTTACAGCCC 1920  
Db 1861 CATCTTAAAGTATGATTTGATATAATCTTATTGAAATTTACCTTTATCATGCTTACAGCCC 1920  
Qy 1921 GTCCTTATGTTTAAACTAATTTCTTAAATTAAGCCCTTCAAGTAAATGTTTCAATACCAAC 1980  
Db 1921 GTCCTTATGTTTAAACTAATTTCTTAAATTAAGCCCTTCAAGTAAATGTTTCAATACCAAC 1980  
Qy 1981 TTGATAAATGCTACTCATAAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTTTTA 2040  
Db 1981 TTGATAAATGCTACTCATAAAGAGCTGGTTGGGCTATAGCATATGCTTTTTTTTTTTA 2040  
Qy 2041 ATTATTACCTGATTTTAAATCTCTGTAAACCGTGTAGTGTCTTCAATAAATCTGTAAC 2100  
Db 2041 ATTATTACCTGATTTTAAATCTCTGTAAACCGTGTAGTGTCTTCAATAAATCTGTAAC 2100  
Qy 2101 CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTTA 2160  
Db 2101 CGCATTTTAAATGATCCGCTATTATAAGCTTTTAAAGCTTTTAAAGCTTTTAAAGCTTTA 2160  
Qy 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTTGCTTG 2220  
Db 2161 ACATTGCCACTTCAACTCTAAGGAATATTTTGGAGATATCCCTTTGGAAGACCTTTGCTTG 2220  
Qy 2221 GAAGAGCTGGACACTTAACTTACACCAAAATTTGCTCTTCAAAATACGTTATGCACTGG 2280  
Db 2221 GAAGAGCTGGACACTTAACTTACACCAAAATTTGCTCTTCAAAATACGTTATGCACTGG 2280  
Qy 2281 ATAACTCTGAGAAACACATCTAGTATAAAGTAAAGAGAGCATCAAAATTAACAGACA 2340  
Db 2281 ATAACTCTGAGAAACACATCTAGTATAAAGTAAAGAGAGCATCAAAATTAACAGACA 2340  
Qy 2341 GAAACCCGAAAGCTCTATATAAATGCTCAGAGTCTCTTTATGTTCTTATTTGCAATTCAA 2400  
Db 2341 GAAACCCGAAAGCTCTATATAAATGCTCAGAGTCTCTTTATGTTCTTATTTGCAATTCAA 2400



QY 2401 CATATGTAATATCAGAAACAGGAAATTTTCATTAATAATATGGTTGAAAT 2454  
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Db 2401 CATATGTAATATCAGAAACAGGAAATTTTCATTAATAATATGGTTGAAAT 2454

## RESULT 14

US-10-137-865-327  
: Sequence 327, Application US/10137865  
: Publication No. US20030032155A1  
: GENERAL INFORMATION:  
: APPLICANT: Baker, Kevin P.  
: APPLICANT: Beresini, Maureen  
: APPLICANT: DeForge, Laura  
: APPLICANT: Desnoyers, Luc  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Gao, Wei-Qiang  
: APPLICANT: Gerritsen, Mary E.  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul J.  
: APPLICANT: Gurney, Austin L.  
: APPLICANT: Sherwood, Steven  
: APPLICANT: Smith, Victoria  
: APPLICANT: Stewart, Timothy A.  
: APPLICANT: Tumas, Daniel  
: APPLICANT: Watanabe, Colin K  
: APPLICANT: Wood, William  
: APPLICANT: Zhang, Zemin  
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
: FILE OF INVENTION: ACIDS ENCODING THE SAME  
: FILE REFERENCE: P3330R1C154  
: CURRENT APPLICATION NUMBER: US/10/137.865  
: CURRENT FILING DATE: 2002-05-03  
: Prior Application removed - See Palm or File Wrapper  
: NUMBER OF SEQ ID NOS: 550  
: SEQ ID NO 327  
: LENGTH: 2454  
: TYPE: DNA  
: ORGANISM: Homo Sapien  
US-10-137-865-327

Query Match 100.08; Score 2454; DB 9; Length 2454;  
Best Local Similarity 100.08; Pred. No. 0;  
Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 GGACTAATCTCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACACAGGACT 60  
|||||  
1 GGACTAATCTCTGGGAGCAGTTTATCCAGTATCACCCAGGGTGCAGCCACACACAGGACT 60  
|||||  
61 GTGTGAAGGGTGTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120  
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61 GTGTGAAGGGTGTTTTTTCTTTTAAATGTAATACCTCCTCATCTTTCTTCTTACAC 120  
|||||  
121 AGTGTCTGAGAACATTTACATATATAGATAAGTAGTACATGTTGGTAACTTCTACTTTTA 180  
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121 AGTGTCTGAGAACATTTACATATATAGATAAGTAGTACATGTTGGTAACTTCTACTTTTA 180  
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181 GGAGGACTACTCTCTCTGACAGCTCTAGCTGTCTTCTACACTAAGACACACATGAAGG 240  
|||||  
181 GGAGGACTACTCTCTCTGACAGCTCTAGCTGTCTTCTACACTAAGACACACATGAAGG 240  
|||||  
241 AGTATGTCTCTCTATTAFTTCTGGCTTTGGCTCTGCGAAACCCCTCTTTTAGCCCTTAC 300  
|||||  
241 AGTATGTCTCTCTATTAFTTCTGGCTTTGGCTCTGCGAAACCCCTCTTTTAGCCCTTAC 300  
|||||  
301 ACATCGCCTGAGAAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATGATG 360  
|||||  
301 ACATCGCCTGAGAAATATGATGCTGAAGGATATGGAAGACACACAGATGATGATGATG 360  
|||||  
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
|||||  
361 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420  
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## RESULT 15

US-10-140-474-327

; Sequence 327, Application US/10140474

; Publication No. US20030032156A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Beresini, Maureen

; APPLICANT: DeForge, Laura

; APPLICANT: Desnoyers, Luc

```
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C162
; CURRENT APPLICATION NUMBER: US/10/140,474
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-140-474-327
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Query Match 100.0%; Score 2454; DB 9; Length 2454;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2454; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: May 31, 2003, 13:43:57  
Job time : 347 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 12:40:22 ; Search time 306 Seconds  
(without alignments)  
2789.240 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1932

Sequence: 1 MKEYVLLFLALCAKPFPS.....PATFRVLSRMSVQLNGFM 379

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Fgapop 6.0 , Fgapext 7.0	
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1992	100.0	2454	20	AA80043	Human PRO241 nucle
2	1992	100.0	2454	22	AA821407	Human CDNA sequenc
3	1992	100.0	2454	24	ABL95575	Human angiogenesis
4	1992	100.0	2454	24	ABL88086	Human PRO241 CDNA
5	1992	100.0	2455	21	AAA49551	Human PRO241 CDNA
6	1968	98.8	1548	22	AAI59507	Human polynucleoti
7	1828	91.8	1492	23	AA86756	DNA encoding novel
8	1799	90.3	2305	22	AA10114	Mouse bone/cartila
9	1799	90.3	2305	24	ABL33045	Murine CDNA isolat
10	1517	76.2	2089	22	AAH18405	Human CDNA sequenc
11	1293	64.9	896	22	AAI94377	Human neuroblastom
12	1225	61.5	854	22	AAH16847	Human CDNA clone (
13	1040.5	52.2	2446	16	AAH0768	Rat biglycan CDNA.
14	1034	51.9	1685	22	AAH07372	Human DNA encoding
15	1034	51.9	1685	22	AAH83977	Human biglycan enc
16	1034	51.9	1685	24	ABL62863	Breast cancer rela
17	1034	51.9	1685	24	ABL63084	Breast cancer rela
18	1034	51.9	1685	24	ABL64383	Stomach cancer rel
19	1034	51.9	2296	24	ABL35121	Human CDNA encodin
20	1034	51.9	2367	20	AAZ53010	Human prostate tum
21	1034	51.9	2384	20	AAZ24428	Human bladder tumo
22	1034	51.9	6321	24	AAZ94760	Human DNA sequence
23	1020	51.2	1685	11	AAQ04490	Sequence encoding
24	1007	50.6	814	22	AAI61293	Human polynucleoti
25	963.5	48.4	1837	20	AAZ41383	Human normal uteru
26	963.5	48.4	2078	20	AAZ41275	Human normal ovari
27	963.5	48.4	2119	23	ABK43616	DNA encoding novel
28	949	47.6	1026	17	AAH10741	Human recombinant
29	949	47.6	2063	23	ABV22279	Human prostate exp
30	949	47.6	2063	23	ABV24765	Human prostate exp
31	949	47.6	2063	23	ABV26594	Human prostate exp
32	949	47.6	2063	23	ABV28113	Human prostate exp
33	948	47.6	2063	23	ABV28779	Human prostate exp
34	948	47.6	4167	21	AAH12499	CDNA encoding a ch
35	947	47.5	1002	14	AAQ50046	Mature decorin pr-
36	947	47.5	4192	17	AAH16517	Collagen A1/decori
37	907	45.5	1593	11	AAQ04491	Sequence encoding
38	906.5	45.5	1997	24	ABK35964	CDNA sequence #355
39	863.5	43.3	1854	22	AAH23087	Osteoarthritis tis
40	847	42.5	924	14	AAQ50053	Decorin (N-termina
41	788.5	39.6	1674	22	AAH33113	DNA encoding human
42	776	39.0	849	14	AAQ50052	Decorin (N-termina
43	616	30.9	711	14	AAQ50051	Decorin (N-termina
44	608	30.5	496	22	AAH81653	Human differential
45	497.5	25.0	505	24	ABL99526	Target canine gene

# ALIGNMENTS

RESULT 1

AA80043

ID AA80043 standard; cDNA; 2454 BP.

XX AA80043;

AC AA80043;

DT 12-AUG-1999 (first entry)

XX Human PRO241 nucleotide sequence.

XX Human; PRO protein; tumour necrosis factor family; TNF; cytokine;

KW secreted protein; transmembrane protein; Inflammation disorder; ss.

XX Homo sapiens.

XX WO9928462-A2.

XX 10-JUN-1999.

PD





QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340  
 DB 1194 AATTCAATTGCAAGAGTGGAGTAATGACTTCTGCCAACAGTGCACAAAGATGAAGAAA 1253  
 QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360  
 DB 1254 TCATTATACAGTGCATAAGTTTATTCAACAACCCGGTGAATACGTGGAAATGCAACCT 1313  
 QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379  
 DB 1314 GCAACATTCGTGTGTTTGGACAGCAATGAGTGTTTCAGCTTGGAACTTTGGAATG 1370  
 RESULT 3  
 ABL95575  
 ID ABL95575 standard; cDNA; 2454 BP.  
 XX AC ABL95575;  
 XX DT 19-JUL-2002 (first entry)  
 XX DE Human angiogenesis related cDNA PRO241 SEQ ID NO: 29.  
 XX KW Human; angiogenesis: PRO protein; cardiovascularisation; wound; cancer;  
 XX OS atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;  
 XX PN cardiant; cyostatic; antiangiogenic; hypotensive; vulnerary;  
 XX PN antiarteriosclerotic; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO200208284-A2.  
 XX PD 31-JAN-2002.  
 XX PF 09-JUL-2001; 2001WO-US21735.  
 XX PR 20-JUL-2000; 2000US-219556P.  
 XX PR 25-JUL-2000; 2000US-220624P.  
 XX PR 28-JUL-2000; 2000US-220664P.  
 XX PR 02-AUG-2000; 2000WO-US20710.  
 XX PR 17-AUG-2000; 2000US-222695P.  
 XX PR 23-AUG-2000; 2000US-0643657.  
 XX PR 24-AUG-2000; 2000WO-US23522.  
 XX PR 07-SEP-2000; 2000WO-US23328.  
 XX PR 15-SEP-2000; 2000US-230978P.  
 XX PR 18-SEP-2000; 2000US-000000P.  
 XX PR 18-SEP-2000; 2000US-0664610.  
 XX PR 18-SEP-2000; 2000US-0665350.  
 XX PR 24-OCT-2000; 2000US-242922P.  
 XX PR 08-NOV-2000; 2000US-0709238.  
 XX PR 10-NOV-2000; 2000WO-US30952.  
 XX PR 01-DEC-2000; 2000WO-US30873.  
 XX PR 20-DEC-2000; 2000WO-US32678.  
 XX PR 20-DEC-2000; 2000US-0747259.  
 XX PR 22-JAN-2001; 2000WO-US34956.  
 XX PR 28-FEB-2001; 2001US-0767609.  
 XX PR 01-MAR-2001; 2001WO-US06520.  
 XX PR 01-MAR-2001; 2001US-0606666.  
 XX PR 14-MAR-2001; 2001US-0802706.  
 XX PR 22-MAR-2001; 2001US-0808689.  
 XX PR 05-APR-2001; 2001US-0816744.  
 XX PR 10-MAY-2001; 2001US-0828366.  
 XX PR 25-MAY-2001; 2001US-0854208.  
 XX PR 25-MAY-2001; 2001US-0866028.  
 XX PR 25-MAY-2001; 2001WO-US17092.  
 XX PR 30-MAY-2001; 2001US-0866034.  
 XX PR 01-JUN-2001; 2001WO-US17092.  
 XX PR 20-JUN-2001; 2001US-0870574.  
 XX PR 28-JUN-2001; 2001WO-US17800.  
 XX PR 28-JUN-2001; 2001US-091692.  
 XX PR 28-JUN-2001; 2001WO-US19000.  
 XX PR 28-JUN-2001; 2001WO-US00000.

(GETH ) GENENTECH INC.  
 PA (BAKE/) BAKER K P.  
 PA (FERR/) FERRARA N.  
 PA (GERB/) GERBER H.  
 PA (GERR/) GERITSEN M E.  
 PA (GODD/) GODDARD A.  
 PA (GODO/) GODOWSKI P J.  
 PA (GURN/) GURNEY A L.  
 PA (HILL/) HILLAN K J.  
 PA (MARS/) MARSTERS S A.  
 PA (PANI/) PAN J.  
 PA (PAON/) PAONI N F.  
 PA (STEP/) STEPHAN J F.  
 PA (WATA/) WATANABE C K.  
 PA (WILL/) WILLIAMS P M.  
 PA (WOOD/) WOOD W I.  
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;  
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;  
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;  
 XX WPI: 2002-171999/22.  
 DR P-PSDB; ABB95437.  
 XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,  
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial  
 PT infarction), endothelial or angiogenic disorders in a mammal -  
 XX Claim 1; Fig 29; 567pp; English.  
 XX The present invention provides the protein and coding sequences of human  
 CC PRO proteins. These are useful for treating or diagnosing a  
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac  
 CC hypertrophy, trauma, cancer, age-related macular degeneration,  
 CC atherosclerosis, hypertension, arterial stenosis, rheumatoid arthritis,  
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour  
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound  
 CC healing. The present sequence is a coding sequence of the invention.  
 XX  
 SQ Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 7.16e-199 Length: 2454  
 Score: 1992.00 Matches: 379  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
 US-09-944-884-2 (1-379) x ABL95575 (1-2454)  
 QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20  
 DB 234 ATGAAGGAGTATGTGCTCTCTATTTCTGCTGCTGCCAACCCCTTTCTTAGC 293  
 QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
 DB 294 CCTTCACACATCGCACTGAGATATGATGCTGGAAGGATATGGAACACACAGATGATGAT 353  
 QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
 DB 354 GAT 413  
 QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80  
 DB 414 CCAAGAAGCCATTTTTCATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 473  
 QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100  
 DB 474 TATTACAGAGTTGTACATGCTCAGATTTAGGTTTGCACCTCAGTCCACACACATTCAC 533  
 QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysLysGluAsnAsp 120  
 DB 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysLysGluAsnAsp 120

Db	534	TTGTACTCGAATGCTTATCTTCAAAACAATAAATAAGGAAATCAAGAAATGAT	593	OS	Homo sapiens.
Qy	121	PheLysGlyLeuThrSerLeuTyrGlyLeuLeuAsnAsnLysLeuThrLysIle	140	PN	WO200200690-A2.
Db	594	TTTAAAGGACTCACTTCACTTTATGCTGATCCTGAACAACAACAGCTAACGAGATT	653	XX	03-JAN-2002.
Qy	141	HisProLysAlaPheLeuThrLysLysLeuArgLeuTyrLeuSerHisAsnGln	160	PD	
Db	654	CACCCAAAGCCCTTCTAACCAACAAGAGTTGCGAGGCTGTATCTGTCCCAATCAA	713	XX	20-JUN-2001; 2001WO-US19692.
Qy	161	LeuSerGluLeuProLeuAsnLeuProLysSerLeuAlaGluLeuHisGluAsn	180	XX	23-JUN-2000; 2000US-213637P.
Db	714	CTAAGTCAATACCACTTAATCTCCCAATCATATAGCAAACTCAGAATTCATGAAT	773	PR	20-JUL-2000; 2000US-219556P.
Qy	181	LysValLysLysIleGlnLysAspThrPheLysLysMetAsnAlaLeuHisValLeuGlu	200	PR	25-JUL-2000; 2000US-220624P.
Db	774	AAAGTTAAGNAATACAAAGGACACATTCAAAGGAATGATGCTTTACACGTTTGAA	833	PR	25-JUL-2000; 2000US-220664P.
Qy	201	MetSerAlaAsnProLeuAspAsnGlyIleGluProGlyAlaPheGluGlyValThr	220	PR	28-JUL-2000; 2000WO-US20710.
Db	834	ATCAGTCAAAACCTCTTGATATAATGGGATAGACGAGCGCATTTGAAGGGTGACG	893	PR	02-AUG-2000; 2000US-222695P.
Qy	221	ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro	240	PR	17-AUG-2000; 2000US-0643657.
Db	894	GTCTTCATATCAGATTGAGAGCAAACTGACCTCAGTTCTTAAAGGCTTACCACCA	953	PR	23-AUG-2000; 2000WO-US23522.
Qy	241	ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe	260	PR	24-AUG-2000; 2000WO-US23328.
Db	954	ACTTATGGAGCTTCACTTAGATTATATAAATTTCAACAGTGAACCTTGAGGATTT	1013	PR	07-SEP-2000; 2000US-230978P.
Qy	261	LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu	280	PR	18-SEP-2000; 2000US-0664610.
Db	1014	AAACGATACAAAGAACTACAAAGGCTGGGCTAGCAAAACAACAATCACAGATATCGAA	1073	PR	18-SEP-2000; 2000US-0665350.
Qy	281	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu	300	PR	24-OCT-2000; 2000US-242922P.
Db	1074	AATGGGAGTCTTGCTAATACATACCACGCTGAGAGAAATACATTTGGAAACAATAACTA	1133	PR	08-NOV-2000; 2000WO-US30952.
Qy	301	LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIlePheLeuHisSer	320	PR	10-NOV-2000; 2000WO-US30873.
Db	1134	AAAAAATCCCTCAGATTACCAAGTGAATGAATACCTCCAGATAATCTCTCATCT	1193	PR	01-DEC-2000; 2000WO-US32678.
Qy	321	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340	PR	20-DEC-2000; 2000US-0747259.
Db	1194	AATCAATTCAAGAGTGGGAGTAGTAATGACTTCTGTCCACAGTGCCAAAGATGAAGAA	1253	PR	20-DEC-2000; 2000WO-US34956.
Qy	341	SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetClnPro	360	PR	22-JAN-2001; 2001US-0767609.
Db	1254	TCATTATACAGTGCATTAAGTTTATTCAACAACCCGGTGAATATCTGGGAATGCAACCT	1313	PR	28-FEB-2001; 2001US-0796498.
Qy	361	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet	379	PR	28-FEB-2001; 2001WO-US06520.
Db	1314	GCAACATTTCTGTGTTTGGAGCAGAAATGAGTGTTCAGCTTGGGAATTTGGAAATG	1370	PR	01-MAR-2001; 2001WO-US06666.
RESULT 4				PR	09-MAR-2001; 2001US-0802706.
ABL88086				PR	14-MAR-2001; 2001US-0808689.
ID	ABL88086	standard; cDNA; 2454 BP.		PR	22-MAR-2001; 2001US-0816744.
AC	ABL88086;			PR	05-APR-2001; 2001US-0828366.
XX				PR	10-MAY-2001; 2001US-0854208.
XX				PR	10-MAY-2001; 2001US-0854280.
DT	16-MAY-2002 (first entry)			PR	25-MAY-2001; 2001US-0866028.
XX				PR	25-MAY-2001; 2001US-0866034.
XX				PR	25-MAY-2001; 2001WO-US17092.
DE	Human PRO241 cDNA sequence SEQ ID NO:29.			PR	30-MAY-2001; 2001US-0870574.
KW	Human: angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;			PR	01-JUN-2001; 2001WO-US17443.
KW	vulnery; antiarteriosclerotic; PRO agonist; PRO antagonist; trauma;			XX	(GETH ) GENENTECH INC.
KW	gene therapy; cardiovascular disorder; endothelial disorder; cancer;			XX	Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
KW	angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;			PI	Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
KW	age-related macular degeneration; arterial restenosis; angina;			PI	Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
KW	rheumatoid arthritis; myocardial infarction; thrombophlebitis;			XX	WPI; 2002-090516/12.
KW	lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;			DR	P-PSDB; ABB84831.
KW	wound healing; chromosome mapping; gene mapping; gene; ss.			DR	One hundred and eighty seven nucleic acids encoding PRO polypeptides,
XX				XX	useful in diagnosis and treatment of cardiovascular (e.g. myocardial
XX				PT	infarction), endothelial or angiogenic disorders in a mammal -
XX				PT	Claim.2; Fig 29; 565pp; English.
XX				PS	ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
XX				CC	ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
XX				CC	antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
XX				CC	activities, and can be used in gene therapy. The PRO polynucleotides,
XX				CC	proteins, agonists and antagonists are useful for treating or diagnosing
XX				CC	a cardiovascular, endothelial or angiogenic disorder in a mammal,
XX				CC	e.g. cardiac hypertrophy, trauma, cancer, age-related macular
XX				CC	degeneration, atherosclerosis, hypertension, arterial restenosis,
XX				CC	rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis,
XX				CC	lymphangitis, tumour angiogenesis (such as breast carcinoma and liver
XX				CC	carcinoma) and wound healing. The PRO polynucleotides have applications
XX				CC	in molecular biology, including use as hybridisation probes, and in
XX				CC	chromosome and gene mapping. ABL88259 to ABL88267 represent primers and
XX				CC	probes used in the exemplification of the present invention.

XX SQ Sequence 2454 BP; 835 A; 432 C; 417 G; 770 T; 0 other;

Alignment Scores:

Pred. No.: 7.16e-199 Length: 2454

Score: 1992.00 Matches: 379

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 24 Gaps: 0

US-09-944-884-2 (1-379) x ABL88086 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLeuLysProPhePheSer 20

DB 234 ATGAGGAGTATGCTCCTTATTTCTGCTTTGCTGCTGCAACCCCTCTTTAGC 293

QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40

DB 294 CCTTCACATCGCACTGAACAATATGATGCTGAGGATATGGAGACACACATGATGAT 353

QY 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60

DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413

QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysPropheGlyCysGlnCys 80

DB 414 CCAAGAACCCATTTTTCATTTGATGCTGTTTCCAAATGTTCCATTTGATGTCAGTGC 473

QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100

DB 474 TATTCACGAGTGTACATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 533

QY 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120

DB 534 TTTGATACCTCAATGCTTCTTCAACCAATAAATTAAGGAATCAAGAAATGAT 593

QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140

DB 594 TTTAAAGGACTCACTTCACTTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 653

QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160

DB 654 CACCAAAAGCCTTCTTCAACCAACAAGATGCGAAGGCTGATCTGCTCCCAATCAA 713

QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180

DB 714 CTAAGTGAAATACCACTTAATCTTCCCAATCATTAGCAGAACTCAGAAATTCATGAAAT 773

QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200

DB 774 AAGTTAAGAAATACAAAAGGACACATTCAGGAATGAATGCTTTTACACGTTTTCGAA 833

QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220

DB 834 ATGAGTGCAACCTCTTGATATATATGATGATGATGATGATGATGATGATGATGATGAT 893

QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240

DB 894 GTGTTCCATATACAGATTCAGAAAGCAAACTGACCTCAGTTCTTCTTAAAGCCTTACCACCA 953

QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuAspPhe 260

DB 954 ACTTTATGAGCTTCACTTAGATATATATAAATTTCAACAGTGGAACTTGGAGATTTT 1013

QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280

DB 1014 AAACGATCAAAAGCACTACAAAGCTGGGCTAGGAACAAACAAATACAGATATCGAA 1073

QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300

DB 1074 AATGGGAGTCTTGCTAACATACCACCTGCTGAGAGAAATACATTTGGAAACATAACTA 1133

QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320

DB 1134 AAAAAATCCCTTCAGGATTACCAGATTGAAATACCTCCAGATAATCTTCTTCATTCT 1193

QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340

DB 1194 AATTCATTTGCAAGAGTGGGAGTAATGACTTCTGTCCAACAGTCCCAAGATGAAGAA 1253

QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360

DB 1254 TCTTTATACAGTGCATTAAGTTTATTCAACACCCGGTGAATACTGGGAATGCAACT 1313

QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379

DB 1314 GCAACATTTGCTGTGTTTGGAGCAAGATGAGTGTTCAGCTTGGGAACCTTTGGAATG 1370

RESULT 5

AAAA9551

ID AAA49551 standard; cDNA; 2455 BP.

XX

AC AAA49551;

XX

DT 25-SEP-2000 (first entry)

XX

DE Human PRO241 cDNA.

XX

KW PRO: membrane bound protein; secreted protein; PRO357; PRO327;

KW PRO243; PRO715; PRO241; PRO323; PRO299; PRO233; PRO344; PRO347;

KW PRO355; PRO353; PRO361; PRO365; transmembrane polypeptide;

KW antibody; screening; detection; inhibition; probe; primer; human;

ss.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 234..1373

FT /\*tag= a

FT /product= PRO241 polypeptide

XX

PN WO200032776-A2.

XX

PD 08-JUN-2000.

XX

PF 01-DEC-1999; 99WO-US28301.

XX

PR 01-DEC-1998; 98WO-US25108.

PR 16-DEC-1998; 98US-0112850.

PR 22-DEC-1998; 98US-0113296.

XX

PA (GETH ) GENENTECH. INC.

XX

PI Baker KP, Botstein D, Eaton DL, Ferrara N, Filvaroff E;

PI Gerritsen ME, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL;

PI Hillan KJ, Kljavin IJ, Napier MA, Roy MA, Tumas D, Wood WI;

XX

DR WPI; 2000-412324/35.

DR P-PSDB; AAB01311.

XX

PT New human nucleic acids encoding secreted and transmembrane

PT polypeptides, designated as PRO polypeptides, useful as pharmaceutical

PT and diagnostic agents

XX

PS Claim 2; Fig 1; 187pp; English.

XX

CC New human nucleic acids encoding secreted and transmembrane

CC polypeptides which are designated as PRO polypeptides are described

CC The membrane-bound proteins have various industrial applications,

CC including as pharmaceutical and diagnostic agents. The membrane-bound

CC proteins can also be employed for screening of potential peptide or

CC small molecule inhibitors of the relevant receptor/ligand interaction.

CC Anti-PRO antibodies are useful for the affinity purification of PRO

CC from recombinant cell culture or natural sources.

XX



SQ Sequence 2455 BP; 836 A; 432 C; 417 G; 770 T; 0 other;

Alignment Scores:  
Pred. No.: 7,16e-199 Length: 2455  
Score: 1992.00 Matches: 379  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 21 Gaps: 0

US -09-944-884-2 (1-379) x AAA49551 (1-2455)

Qy 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20  
Db 234 ATGAAGGATGATGTCTTCATTATTTCCCTGGCTTTTGCTCTGCCAAACCTCTCTTTAGC 293  
21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
294 CCTCACATCCCATCGAAGTAATGATGCTGAAGGATATGGAACACACAGATGATGAT 353  
41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413  
61 ProArgSerHisPheProPhePhePhePhePhePhePhePhePhePhePhePhePhe 80  
414 CCAAGAAGGCATTTTTTCCATTTGATCTGTTTCCAATGTGCCATTTGGATGTCAGTGC 473  
81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100  
474 TATTCAGAGTGTACATGCTCAGATTTAGTTTGGCTCAGTCCCACCAACATTCACA 533  
101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120  
534 TTTGATACTCGAATGCTTGATCTTCAAACAATAAAATTAAGSAAATCAACAAAAATGAT 593  
121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnAsnLysLeuThrLysIle 140  
594 TTTAAAGGACTCACTTCACTTTATGTGCTGATCCTGAACAACAAGCTAACGAAGATT 653  
141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160  
654 CACCAAAAGCCCTTCTAACCAAGAAGTTCGGAAGCTGTATCTGTCCCAACATCAA 713  
161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
714 CTAAAGTAATACCCTTAATCTTCCCAATCATTAGCAGAACTCAGAAATTCATGAAAT 773  
181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200  
774 AAAGTTAAGAAAATACAAAAGGACACATTAAGGAATGAATGCTTTACACGCTTTTGGAA 833  
201 MetSerAlaAsnProLeuAspAsnAngIleGluProGlyValAlaPheGluGlyValThr 220  
834 ATGAGTCCAAACCTCTTGATAATATGGAATAGACCCAGGGGCATTTGAAGGGGTGACG 893  
221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240  
894 GTGTTCATATCAGATTCAGAAAGCAAACTGACCTCAGTCTTAAAGGCTTACACCA 953  
241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260  
954 ACTTTATTGGAGCTTCACTTAGATTTATATAAAATTTCAACAGTGGAACTTCAGGATTTT 1013  
261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280  
1014 AAACGATACAAAGAACTTACAAAGGCTGGGCTAGGAAACAACAAATTCAGATTCGAA 1073  
281 AsnClySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300  
1074 AATGGGAGCTTGTACATACACACGCTGTGAGAGAATACATTTGGAAACAATAAATCA 1133  
301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320



a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention. CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at ftp.wipo.int/pub/published\_pct\_sequences.

Sequence 1492 BP; 499 A; 279 C; 279 G; 435 T; 0 other;

# Alignment Scores:

Pre-d. No.: 5, 89p-182 Length: 1492  
 e: 1828.00 Matches: 374  
 .ent Similarity: 96.41% Conservative: 2  
 Best Local Similarity: 95.90% Mismatches: 2  
 Query Match: 91.77% Indels: 12  
 DB: 23 Gaps: 1

US-09-944-884-2 (1-379) x AAS86756 (1-1492)

QY 2 LysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProphe-PheSerP 21  
 Db 236 AAGGAGTATGCTCCTAATATTCTGCTTGGCTCTGCAAAACCTTCCTTACGCC 295  
 QY 21 roSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetClnuAspThrAspAspa 41  
 Db 296 CTTACACATCGCCTCAAGAAATATGATGCTGAAGGATATGAAGACACAGATGATGAGG 355  
 QY 41 sp-----AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrA 59  
 Db 356 ATGACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 415  
 QY 59 rgGluProArgSerHis-PhePheProPheAspLeuPhePrometCysProPheGlyCys 78  
 Db 416 GAGAGCCCAAGAGCCATTTTTCCTATTTGATCTGTTTCCCAATGTCCTCATTTGGATGT 475  
 QY 79 GlnCysTyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsn 98  
 Db 476 CAGTGTATATTCAGAGTGTACATTTGCTCAGATTTAGTTTGGACCTCAGTCCCAACCAAC 535  
 Db 99 IleProPheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGlu 118  
 Db 536 ATTCCATTGTACTCGAATGCTTCTTCAACACATATAAATTAAGGAATCAAGNA 595  
 QY 119 AsnAspPheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThr 138  
 Db 596 AATGATTTTAAAGGACTCACTTCACCTTTATGCTCTGATCCTGAACAACAACAAGCTAACG 655  
 QY 139 LysIleHisProLysAlaPheLeuThrLysLysLysLeuArgArgLeuTyrLysSerHis 158  
 Db 656 AAGATTCCACCAAAAGCCCTTCTAACCACAAAGAAGTTGCGAAGGCTGTATCTGTCACAC 715  
 QY 159 AsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHis 178  
 Db 716 AATCAACTAAGTGAATACCACTTAACTTCCCAATCATTTAGCAAGCTCAGAATTCAT 775  
 QY 179 GluAsnLysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisVal 198  
 Db 776 GAAATTAAGTTAAGAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGTT 835  
 QY 199 LeuGluMetSerAlaAsnProLeu-AspAsnAsn-GlyIleGluProGlyAlaPhe--G1 217  
 Db 836 TTGGAAATCAGTGCACCAACCTCTTTGATATAATATGGGATAGACGAGGGCATTTTGAA 895  
 QY 217 uGlyValThrValPheHisIleArgIleAlaGluAlaLysLeuThrSerVal-Pro-Lys 236  
 Db 896 GGGGTGAGGGTGTTCATATCAGATTCAGAAATTCAGAAACAAACTGACCTCAGTTTCTCTAAG 955

QY 237 GlyLeuProProThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGlu 256  
 Db 956 GGCTTACCACCAACTTTATTGGAGCTTCACATTAGATAATAAAATTTCAACAGTGGAA 1015  
 QY 257 LeuGluAspPheLysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIle 276  
 Db 1016 CTTGAGGATTTTAAACGATACAAGAACTACAAGGCTGGCCCTTAGGAAACAACAATC 1075  
 QY 277 ThrAspIleGluAsnGlySerLeuAlaAsnIleProArgValArg-GluIleHisLeuG1 296  
 Db 1076 ACAGATATCGAAATGGGAGTCTTGTCTAACATACCACTGTCGAGGAGAGATACATTTGGG 1135  
 QY 296 uAsnAsnLysLeuLysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIle1 316  
 Db 1136 AACATTAACATAAAAAAATCCCTTCAGGATTAACAGAGTTGAATACCTCCAGATAAT 1195  
 QY 316 ePheLeuHisSerAsnSerIleAlaArgValGlyValAsnAspPheCysProThrValPr 336  
 Db 1196 CTTCTTCATCTTAATCAATGCAAGAGTGGAGTAATACATCTCTCCCAACAGTCC 1255  
 QY 336 oLysMetLysLysSerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTr 356  
 Db 1256 AAAGATGAAGAAATCTTTATACAGTGCATAAAGTTTATTCAACACCCGGTGAATACTG 1315  
 QY 356 pGluMetClnProAlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAs 376  
 Db 1316 GGAATGCAACCTGCAACATTTCTGTTGTGTTGAGCAGAATGAGTGTTCAGCTTTGGGAA 1375  
 QY 376 nPheGlyMet 379  
 Db 1376 CTTTGGAAATG 1385  
 RESULT 8  
 AAD10114  
 ID AAD10114 standard; cDNA; 2305 BP.  
 XX AAD10114;  
 AC AAD10114;  
 DT 12-SEP-2001 (first entry)  
 XX Mouse bone/cartilage proteoglycan I (BGN) cDNA.  
 DE Mouse; cytostatic; antiinflammatory; immunoregulatory; tissue integrity;  
 KW Mouse healing; immune response; vaccine; cancer; asthma; allergy;  
 KW cell trafficking; BGN; bone/cartilage proteoglycan I protein;  
 KW biglycan; PG-S1; secreted protein; therapy; ss.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 238..1359  
 FT /\*tag= a  
 FT /product= "Mouse bone/cartilage proteoglycan I"  
 XX WO200148192-A1.  
 PN  
 XX  
 PD 05-JUL-2001.  
 XX  
 PF 21-DEC-2000; 2000WO-NZ00256.  
 XX  
 PR 23-DEC-1999; 99US-0171678.  
 PR 28-NOV-2000; 2000US-0724864.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 XX  
 PI Watson-JD, Murison JG;  
 XX  
 DR WPI; 2001-425665/45.  
 DR P-PSDB; AAE05347.  
 XX  
 PT Novel isolated polypeptide useful to isolate corresponding interacting  
 PT proteins or other compounds, to quantitatively determine levels of  
 PT interacting proteins or other compounds, and as therapeutic target

Db	640	CACCCAAAACCTTTCTAACCAAGAAATTTGAGAAGGCTATATTTATCCACAACCAA	699
Qy	161	LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn	180
Db	700	CTAAGTGAATTTCCACTTAATCTTCCCAANTCATTTAGCAGAACTCAGAATTCATGATAAT	759
Qy	181	LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu	200
Db	760	AAAGTTAAGAAGATACAAAGGACACGTTCAAGGGAATCAATGCTTTACATGTTTTGGAA	819
Qy	201	MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr	220
Db	820	ATGAGTGCAACCTCTTGAGAACACGGGATAGAACACAGGGGCATTTCGAAGGGGTGACA	879
Qy	221	ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro	240
Db	880	GTATTCCATATCAGGATCGCTGAAGCAAAACAACTCAATTCCCAANGCGCTACACCA	939
Qy	241	ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe	260
Db	940	ACTTTGCTGGAGCTTCATTTAGATTTTAAATAAATTTCAACGGTGGAACTTGAAGATCTT	999
Qy	261	LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu	280
Db	1000	AAACGGTACAGGGAACTCGAAGGCTGGCTCTGGAAACAACAGATATCAGATATTGAA	1059
Qy	281	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu	300
Db	1060	AATGGAACTTTTGCTTAATATACCACGCTGTGAGAGAGATACACTTGGCAACCAATAAACA	1119

QY 301 LYSIIEPROSERCYLeuPROGluLeuLysTYRLeuGlnHIEIlePheLeuHisser 320

DB 1120 AAAAAAATCCCTTCAGGATTACAGGAGTTGAAATACCTCCAGATAATCTTCCATCATTAAT 1179

[illegible]

DB 1240 TCTTTATACAGTGGCAATTAAGTTTATTCACACAACCCCAATGAAGTACTGGGAAAATACAACT 1299

Dc		1300	GCAACAATTCGTTGTCTTGGCACAATGAGTGTTACAGCTTGGGAATGTTGA	1353
 RESULT 9				
ABL35045	ID	ABL35045 standard; cDNA; 2305 BP.		
XX	XX	AC AC		
XX	XX	ABL35045;		
DT	04-APR-2002	(first entry)		
XX	XX	Murine cDNA isolated from skin cells SEQ ID NO: 574.		
DE	XX	Human; rat; mouse; skin cell; skin wound; cancer; growth defect;		
KW	KW	developmental defect; inflammatory disease; dermatological; vulnery;		
KW	KW	immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;		
KW	SS.	ss.		
OS	XX	Mus sp.		
XX	XX			
PN	WO200190357-A1.			
XX	XX			
PD	29-NOV-2001.			
XX	XX			
PF	24-MAY-2001; 2001WO-NZ00099.			
XX	XX			
PR	24-MAY-2000; 2000US-206650P.			
PR	25-JUL-2000; 2000US-221232P.			
XX	XX			
PA	(GENE-) GENESIS RES & DEV CORP LTD.			

## RESULT 9

ABL35045  
ID ABL35045 standard; cDNA: 2305 BP.

XX ABL35045: AC

AC  
XX  
XX  
DT 04-APR-2002 (first entry)

XX  
DE  
Murine cDNA isolated from skin cells SEO ID NO: 574.

Human; rat; mouse; skin cell; skin wound; cancer; growth defect;  
developmental defect; inflammatory disease; dermatological; vulnery;  
immunomodulator; anti-inflammatory; cytostatic; neuroprotective; gene;  
ss.

XX  
OS  
Mus sp.

XX  
PN WO200190357-A1

FN XX  
MOZ0019035/-A1.

PD 29-NOV-2001.

[illegible]

PF 24-MAY-2001; 2001WO-NZ00099.

XX  
PR 24-MAY-2000: 2000US-206650P

PR 25-JUL-2000; 2000US-221232P.  
PR 25-JUL-2000; 2000US-221232P.  
PR 25-JUL-2000; 2000US-221232P.

[illegible]

PA (GENE-) GENESIS RES &amp; DEV CORP LTD.





XX WPI: 2001-565584/63.  
 XX Nucleic acids originating in gene expressed in human neuroblastoma,  
 PT useful as probe or primer in diagnosing prognosis of human  
 PT neuroblastoma, malignancy and susceptibility indicator or tumour marker  
 PT for anti-cancer agents -  
 XX  
 XX Claim 1: Page 377; 2979pp; Japanese.  
 XX  
 CC The invention relates to novel genes (AAI93926-AAI97963) expressed in  
 CC human neuroblastoma. The nucleic acids are applicable as a probe or  
 CC primer in diagnosing the prognosis of human neuroblastoma, malignancy and  
 CC susceptibility indicators or tumour markers for anti-cancer agents. The  
 CC gene information for diagnosing prognosis is related to factors similar  
 CC to that for N-myc and TrkA genes.  
 YV Sequence 896 BP; 340 A; 169 C; 162 G; 216 T; 9 other;  
 Alignment Scores:  
 Pred. No.: 4,15e-126 Length: 896  
 Score: 1293.00 Matches: 263  
 Percent Similarity: 95.32% Conservative: 2  
 Best Local Similarity: 94.60% Mismatches: 10  
 Query Match: 64.91% Indels: 3  
 DB: 22 Gaps: 0  
 US-09-944-884-2 (1-379) x AAI94377 (1-896)  
 QY 105 MetLeuAspLeuGlnAsnAsnLysLysGluIleLysGluAsnAspPheLysGlyLeu 124  
 DB :::: 21 CTACTGGATCTTCAAAACAATAAATAAGGAATCAAGAAATGATTTAAAGGACTC 80  
 QY 125 ThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLysLeuThrLysLysIleHisProLysAla 144  
 DB :::: 81 ACTTCACTTATGCTGTGATCTCTGACACACACACAGCTACCAAGATTCACCCAAAGCC 140  
 QY 145 PheLeuThrThrLysLysLeuArgLysLeuSerHisAsnGlnLeuSerGluIle 164  
 DB :::: 141 TTTCTAACCAACAAGAAGTTGCGAAGGCTGTATCTGTCACCAATCAACTAAGTGAATA 200  
 QY 165 ProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsnLysValLysLys 184  
 DB :::: 201 CCACCTTAATCTTCCCAATCATAGCAGAACCTACAGAAATTCATGAAATTAAGTAAAGAA 260  
 DB :::: 185 IleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuLeuMetSerAlaAsn 204  
 DB :::: 261 ATACAAAAGGACACATCAAGGAATGAATGCTTTTACACGTTTGGAAATGAGTGCACAA 320  
 QY 205 ProLeuAspAsnGlnLysIleGluProGlyValAlaPheGluGlyValThrPheHisIle 224  
 DB :::: 321 CCTCTTGATTAATATGCGATAGCCAGCGGGCATTTGAAGGGGTGACGGTGTTCATATC 380  
 QY 225 ArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProProThrLeuLeuGlu 244  
 DB :::: 381 AGAATTCAGAGCAAAACAGCTCAGTTCTCTAAAGGCTTACCACCACTTTATTGGAG 440  
 QY 245 LeuHisLeuAspTyrAsnLysIleSerThrValGluLeuLysPheLysArgTyrLys 264  
 DB :::: 441 CTTCACTTAGATATATATAAATTTCAACAGTGAACCTTCAGGATTTTAAACGATACAA 500  
 QY 265 GluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsnGlySerLeu 284  
 DB :::: 501 GAACATCAAGGCTGGCGCTTAAGAACACAAACAAATCACAGATATCCAAATGGGACTCCT 560  
 QY 285 AlaAsnIleProArgValArg-GluIleHisLeuGluAsnAsnLysLeuLysLysIlePr 304  
 DB :::: 561 GCTAACATACCAGCTGTGAGAGAAATACATTTGGCAAAACATAAATAAATAAATCC 620  
 QY 304 OSerGlyLeuPro-GluLeuLysTyrLeuGln-IleIlePheLeuHisSerAsnSerIle 323  
 DB :::: 621 TTCAGGATTACCAAGAGTTGAATACCTCCAGATAATCTCCTTCANTCCAATTCAT 680

QY 324 AlaArgValGlyValAsnAspPheCysProThrValProLysMetLysSerLeuTyr 343  
 DB :::: 681 GCAAGAGTGGAGTAATGACTTCTCTCAACAGAGTCCCAAGATGAAGAAATCCTTATAC 740  
 QY 344 SerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAlaThrPhe 363  
 DB :::: 741 AGTGCATTAAGTTTANTCAACACCCNGTGAATACTGGAAATGCAACTGCCAACANTT 800  
 QY 364 ArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379  
 DB :::: 801 CGTGGGGTTTTCAGCAAAATGAGTGTCAACTTGGCAACNTTGGNATG 848  
 RESULT 12  
 AAH16847  
 ID AAH16847 standard; cDNA; 854 BP.  
 XX AAH16847;  
 AC  
 XX 26-JUN-2001 (first entry)  
 DT Human cDNA clone (5'-primer) SEQ ID NO:16124.  
 XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.  
 XX Homo sapiens.  
 OS  
 XX EP1074617-A2.  
 PN  
 XX 07-FEB-2001.  
 PD  
 XX 28-JUL-2000; 2000EP-0116126.  
 PF  
 XX 29-JUL-1999; 99JP-0248036.  
 PR 27-AUG-1999; 99JP-0300253.  
 PR 11-JAN-2000; 2000JP-0118776.  
 PR 02-MAY-2000; 2000JP-0183767.  
 PR 09-JUN-2000; 2000JP-0241899.  
 XX  
 XX (HELI-) HELIX RES INST.  
 XX  
 XX Ota T, Isoqai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX  
 XX WPI: 2001-318749/34.  
 DR  
 XX Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 PS  
 XX Claim 1; SEQ ID 16124; 2537pp + CD ROM; English.  
 XX  
 CC The present invention describes primer sets for synthesising 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dr primer and an oligonucleotide complementary  
 CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesising polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to  
 CC AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification

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CC of the present invention.
XX
SQ Sequence 854 BP; 281 A; 166 C; 162 G; 242 T; 3 other;

Alignment Scores:      5,33e-119      Length:      854
Pred. No.:      1225.00      Matches:      235
Score:      96.33%      Conservative:      1
Percent Similarity:      95.92%      Mismatches:      5
Best Local Similarity:      61.50%      Indels:      4
Query Match:      22      Gaps:      1
DB:

US-09-944-884-2 (1-379) x AAH16847 (1-854)
QY      1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
DB      92 ATCAAGGAGTATGTGCTCTCTATATTCTGGCTTGTCTGCCAACCCTTCTTTAGC 151
QY      21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThr----- 37
DB      152 CTTTCACACATGCCACTGAAGATATATGCTGCTGAAGATATGAAGACACAGATGATGAT 211
QY      38 ----AspAspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPhe 56
DB      212 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 271
QY      57 ProThrArgGluProArgSerHisPhePhePheProPheAspLeuPheProMetCysProPhe 76
DB      272 CCAACAAGAGAGCAAGAAGCCATTTTTCATTTTCATTTTCATTTTCATTTTCATTTTC 331
QY      77 GlyCysGlnCysTyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValPro 96
DB      332 GGATGTCAGTGTCTATTCACAGGTGTACATTTGCTCAGATTTAGTTTGCCTCAGTCCCA 391
QY      97 ThrAsnIleProPheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIle 116
DB      392 ACCAACATTCATTTGATCTGATCTTCAAAACAATAAAATTAAGGAATC 451
QY      117 LysGluAsnAspPheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLys 136
DB      452 AAAGAAAATGATTTTAAAGGACTCACTTCACTTTATGCTGTGATCTCTGAAACAACAAG 511
QY      137 LeuThrLysIleHisProLysAlaPheLeuThrLysLysLeuArgArgLeuTyrLeu 156
DB      512 CTACGGAAGATTCACCAAAAGCCTTTCTAACCAAGAAAGTTGCAAGGCTGTATCTG 571
QY      157 SerHisAsnGlnLeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArg 176
DB      572 TCCCAACAATCAACTAAGTGAATACCACCTTAATCTTCCCAATCATTAGCAGAACTCAGA 631
QY      177 IleHisGluAsnLysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeu 196
DB      632 ATTCATGAAAATAAAGTTAAGAAAATACAAAAGACACATTTCAAGGAATGAATGCTTTA 691
QY      197 HisValLeuGluMetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPhe 216
DB      692 CACGTTTGGGAATGATGCAAAACCTCTTGATAAATGGGATAGCCAGGGGATTT 751
QY      217 GluGlyValThrValPheHisIleArgIleAlaIleAlaLysLeuThrSerValProLys 236
DB      752 GAAGGGTGACGGTGTTCATATACAAATTCAGAAATTCAGAAAGCAAAACTGGNCACAGTTCCTAA 811
QY      237 GlyLeuProProThr 241
DB      812 GATAATCTTCCTTCA 826

RESULT 13:
AAT08768
ID AAT08768 standard; cDNA; 2446 BP.
XX
AC AAT08768;
XX
DT 20-MAR-1996 (first entry)

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XX      Rat biglycan cDNA.
DE
XX
KW Biglycan; proteoglycan; chondroitin sulphate; neuron protection;
KW neurotrophic; central nervous system; CNS; memory loss; dementia;
KW learning; ss.
OS Rattus sp.
FH Key
FT 123..1232 Location/Qualifiers
CDS /*tag= a
FT sig_peptide 123..233 /*tag= b
FT mat_peptide 234..1229 /*tag= c
XX
PN W09530432-AL.
XX
PD 16-NOV-1995.
XX
PF 09-MAY-1994; 94WO-EP01479.
XX
PR 09-MAY-1994; 94WO-EP01479.
XX
PA (BOEF ) BOEHRINGER MANNHEIM GMBH.
XX
PI Hasenoechrl R, Huston J, Junghans U, Kappler J, Koops A;
PI Mueller HW;
XX
PI WPI; 1995-403938/51.
XX
DR P-PSDB; AAR87951.
XX
PT Proteoglycan cpds., partic. chondroitin sulphate proteoglycan(s)
PT for maintain structural and function of the CNS and attenuating
PT memory deficit(s) in the elderly and patients with dementia
XX
PS Disclosure; Page 44-45; 60pp; English.
XX
CC A cDNA sequence (AAT08768) obtd. from rat smooth muscle codes for rat
CC biglycan (AAR87951), a chondroitin sulphate proteoglycan with
CC neurotrophic activity for brain neurons. The cDNA may be inserted
CC into a vector and used for prodn. of recombinant biglycan in
CC eukaryotic host cells.
XX
SQ Sequence 2446 BP; 562 A; 768 C; 508 G; 608 T; 0 other;

Alignment Scores:      5.28e-99      Length:      2446
Pred. No.:      1040.50      Matches:      199
Score:      70.37%      Conservative:      67
Percent Similarity:      52.65%      Mismatches:      93
Best Local Similarity:      52.23%      Indels:      19
Query Match:      16      Gaps:      3
DB:

US-09-944-884-2 (1-379) x AAT08768 (1-2446)
QY      4 TyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhe-----Phe 19
DB      135 TGCGTACTACCTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 194
QY      20 SerProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 39
DB      195 TGGGACTTCACCTTGGATGATGGGCTGCTCATGATGATGATGATGATGATGATGATGAT 254
QY      40 AspAspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArg 59
DB      255 GACACCACCTTCAGGTGCTCCTGACCTGGAC-----TCTCTCACCTTACC----- 299
QY      60 GluProArgSerHisPhePhePheProPheAspLeuPheProMetCysProPheGlyCysGln 79
DB      300 -----TTTCAGTGGCCATGTGCTCTTTTGGTGGCCAC 329

```





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Db 451 AAGGGTCTCCAGCAGCTTACGCCCTCGCTGGTGAACAACAGATCTCCAGATCCAT 510
QY 142 ProLysAlaPheLeuThrLysLysLeuArgLeuArgLeuSerHisAsnGlnLeu 161
Db 511 GAGAGGCTTACAGCCACTGCGGAAGCTGCAAGCTTACATCTCCAAGAACCACCTG 570
QY 162 SerGluLeuProLeuAsnLeuProLysSerLeuAlaGluLeuArgLeuHisGluAsnLys 181
Db 571 GTGAGATCCGCGCCCAACCTACCCAGCTCGCTGGTGGAGCTCGGCATCCAGCAACCCG 630
QY 182 ValLysLysLeuGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMet 201
Db 631 ATCCGCAAGTCCCAAGGAGGTTCAGCGGCTCCGCAACATGACTCCATCGAGATG 690
QY 202 SerAlaAsnProLeuAspAsnAsnGlyLeuGluProGlyAlaPheGluGlyValThrVal 221
Db 691 GCGGGAACCCACTGGAGAACAGTGGCTTTGACCTGGAGCTTCGATGGCTGAAGCTC 750
QY 222 PheHisLeuArgLeuAlaGluAlaLysLeuThrSerValProLysGlyLeuProThr 241
Db 751 AACTACTCGGCATCTCAGAGCCCAAGCTGACTGGCATCCCAAGACCTCCCTGAGACC 810
Db 242 LeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLys 261
Db 811 CTGAATGAATCCACCTAGACCAACAATAATCCAGGCCATCGAATCGGAGGACCTGCT 870
QY 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsn 281
Db 871 CGTACTCAAGCTGTACAGGCTGGGCTAGGCCACCAACAGATGATGATGAGAGAAC 930
QY 282 GlySerLeuAlaAsnIleProArgValArgGluLeuHisLeuGluAsnAsnLysLeuLys 301
Db 931 GGGAGCTGAGTCTCTGCCACCTCCCGGAGCTCCACTTGGACAAACAAGTTGGCC 990
QY 302 LysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleLeuPheLeuHisSerAsn 321
Db 991 AGGGTCCCTCAGGGCTCCAGACCTCAAGCTCTCCAGGTGTCTATCTGCACTCCAAC 1050
QY 322 SerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysSer 341
Db 1051 AACATCACCACCAAGTGGGTGTACACGACTTCTGTCCATGGGCTTCGGGGTGAAGCGGCC 1110
QY 342 LeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAla 361
Db 1111 TACTACAGGCAATCAGCTCTTTCACAAACCCCGTCCCTACTGGAGGTGACCGGCC 1170
QY 362 ThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPhe 377
Db 1171 ACTTTCCGCTGGCTCACTGACCGCTGGCCATCCAGTCTTGGCAACTAC 1218

JLT 15
...83977
ID AAF83977 standard; DNA; 1685 BP.
AC
XX
XX AAF83977;
DT 06-AUG-2001 (first entry)
XX
XX Human biglycan encoding nucleotide sequence.
XX
XX Dystrophin-associated protein complex; DAPC; postsynaptic membrane;
KW biglycan; muscular dystrophy; neuromuscular; neurological; smooth muscle;
KW nontropic; neuroleptic; antiviral; ds.
XX
XX Homo sapiens.
XX
XX Key
XX Location/Qualifiers
XX 121..1227
XX /*tag= a
XX
XX WO200136475-A2.
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PD 25-MAY-2001.
XX
XX 17-NOV-2000; 2000WO-US31661.
XX
XX 18-NOV-1999; 99US-0166253.
XX
XX (UYBR-) UNIV BROWN RES FOUND.
XX
XX Fallon J, McKechnie B, Rafil M, Creely H, Bowe M, Ferri R;
XX
XX WPI; 2001-355617/37.
XX
XX P-PSDB; AAB85043.
XX
XX Stabilizing dystrophin-associated protein complexes and activating
XX postsynaptic membrane of a cell for treating or preventing muscular,
XX neuromuscular and neurological disorders, involves contacting cell with
XX biglycan
XX
XX Disclosure; Page 101-108; 112pp; English.
XX
XX The invention relates to stabilizing dystrophin-associated protein
XX complexes (DAPCs) on the surface of a cell or activating a postsynaptic
XX membrane of a cell that comprises contacting the cell with an effective
XX amount of biglycan. A composition comprising biglycan or its portion
XX is useful for treating or preventing a condition associated with abnormal
XX DAPC in cells, characterized by breakdown of muscle cell membrane, which
XX includes muscular dystrophies, such as Duchenne's, Becker's, Congenital,
XX Limb-girdle muscular dystrophy and myotonic dystrophy and a condition
XX characterized by abnormal neuromuscular junction or synapse, such as
XX neuromuscular or neurological diseases in a subject. Neurological
XX disorders, include polymyositis and Alzheimer's disease. Biglycan is also
XX useful for preventing and treating smooth muscle disorders, such as
XX cardiac myopathies and for treating and inhibiting infections of cells by
XX microorganisms e.g. viruses. Agents that modulate the activity of
XX DAG-125, identified by the methods are useful in the prophylactic and
XX therapeutic treatments of diseases or disorders, characterized by an
XX unstable DAPC or an inappropriate formation of a postsynaptic
XX differentiation. Biglycans are also useful as a supplement to brain or
XX muscle cell or tissue culture and, tissues can be incubated in vitro
XX with biglycan to reverse tissue atrophy and to improve their growth or
XX survival in vitro. The present sequence represents a nucleotide sequence
XX encoding human biglycan.
XX
XX Sequence 1685 BP; 357 A; 593 C; 436 G; 299 T; 0 other;
XX
XX Alignment Scores:
XX Pred. No.: 1.52e-98 Length: 1685
XX Score: 1034.00 Matches: 200
XX Percent Similarity: 69.95% Conservative: 63
XX Best Local Similarity: 53.19% Mismatches: 93
XX Query Match: 51.91% Indels: 20
XX DB: 22 Gaps: 3
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Db 139 CTCGTGTCTCTGCTGGCCCTGAGCCGCCCTTTGAGCAGAGAGGCTTCTGGGAC 198
QY 22 SerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAspAsp 41
Db 199 TTCACCTCGAGATGGGCCATTCATGATGACATGAGGAAGCTTCGGGGCTGACACC 258
QY 42 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGluPro 61
Db 259 TCAGGCGCTCTGGACCCGAC-----TCTGTACACACCCACTACAGC--- 300
QY 62 ArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCysTyr 81
Db 301 -----GCCATGTGTCTCTTCGGTGGCCACTGCCAC 330
QY 82 SerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIleProPhe 101
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Db 391 GACACCACGCTGTGTGACCTGCAGAACACAGCATCTCCGAGCTCCGCAAGGATGACTTC 450
QY 122 LysGlyLeuThrSerLeuThrGlyLeuIleLeuAsnAsnLysLeuThrLysIleHis 141
Db 451 AAGGGTCTCCAGCACCTCTACGCCCTCGTCTGGTGAACAACAAGATCTCCAAGATCCAT 510
QY 142 ProLysAlaPheLeuThrLysLysLysLeuArgArgLeuThrLeuSerHisAsnGlnLeu 161
Db 511 GAGAGGGCTTCCAGCCACTCGCGAAGCTGCAGAAGCTTACATCTCCAAGAACCACCTG 570
QY 162 SerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsnLys 181
Db 571 GTGGAGATCCGCCCAACCTTACCACCTCCCTGGTGGAGCTCCGATCCACGACCAACCGC 630
QY 182 ValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGluMet 201
Db 631 ATCCGCAAGGTGCCCAAGGAGTGTTCAGCGGGCTCCGGAACATGAATGCATCGAGATG 690
QY 202 SerAlaAsnProLeuAspAsnGlyIleGluProGlyAlaPheGluGlyValThrVal 221
Db 691 GCGGGAACCCACTGGAGACAGTGGCTTTGAACCTGGAGCTTCGATGGCTGAAGCTC 750
QY 222 PheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProThr 241
Db 751 ACTACTCGGCATCTCAGAGGCCAAGCTGAGTGGATCCCAAGACCTCCCTGAGACC 810
QY 242 LeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPheLys 261
Db 811 CTGAATGAACCTCCACCTAGACCACACAAATCCAGGCCATCCGAGGACCTGCTT 870
QY 262 ArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGluAsn 281
Db 871 CGCTACTCCAAGTGTACAGGCTGGGCTAGGCCACAAACAGATCAGGATGATCGAGAAC 930
QY 282 GlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeuLys 301
Db 931 GGGAGCTGAGCTTCCTGCCCCACCTCCGGGAGCTCCACTGGACACAAACAAGTTGGCC 990
QY 302 LysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSerAsn 321
Db 991 AGGGTCCCTCAGGGCTCCAGACCTCAAGCTCTCCAGGTGGTCTATCTGCACCTCAAC 1050
QY 322 SerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLysSer 341
Db 1051 AACATCACCACAAGTGGGTGTCAACGACTTCTGTCCCATGGGCTTCGGGTGAAGCGGCC 1110
QY 342 LeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnProAla 361
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Search completed: May 31, 2003, 15:45:08

Job time : 318 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 31, 2003, 15:15:17 ; Search time 205 Seconds  
(without alignments)  
2492.831 Million cell updates/sec

Title: US-09-944-884-2

Perfect score: 1992

Sequence: 1 MKEVLLFLALCSAKPFPS.....PATERCVLSRMSVQLGNEFM 379

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delop 6.0 , Delext 7.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool/US0944884/runat\_27052003\_150250\_7746/app\_query.fasta\_1.519

-DB=PublishedApplications\_NA -QMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62

-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR\_MAX=100

-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTEXT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=2000000000 -USER=US0944884 -CGN\_1\_1\_57 -runat\_27052003\_150250\_7746

-NCPUS=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100

-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5

-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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14: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1992	100.0	2454	9	US-09-944-413-1 Sequence 1, Appli
2	1992	100.0	2454	9	US-09-944-403-1 Sequence 1, Appli
3	1992	100.0	2454	9	US-09-944-896-1 Sequence 1, Appli
4	1992	100.0	2454	9	US-09-944-944-1 Sequence 1, Appli

5	1992	100.0	2454	9	US-09-944-907-1 Sequence 1, Appli
6	1992	100.0	2454	9	US-09-944-929-1 Sequence 1, Appli
7	1992	100.0	2454	9	US-10-028-072-327 Sequence 327, App
8	1992	100.0	2454	9	US-10-121-049-327 Sequence 327, App
9	1992	100.0	2454	9	US-10-123-904-327 Sequence 327, App
10	1992	100.0	2454	9	US-10-140-470-327 Sequence 327, App
11	1992	100.0	2454	9	US-10-175-746-327 Sequence 327, App
12	1992	100.0	2454	9	US-10-176-918-327 Sequence 327, App
13	1992	100.0	2454	9	US-10-176-921-327 Sequence 327, App
14	1992	100.0	2454	9	US-10-137-865-327 Sequence 327, App
15	1992	100.0	2454	9	US-10-140-474-327 Sequence 327, App
16	1992	100.0	2454	9	US-10-142-431-327 Sequence 327, App
17	1992	100.0	2454	9	US-10-143-114-327 Sequence 327, App
18	1992	100.0	2454	9	US-10-140-002-327 Sequence 327, App
19	1992	100.0	2454	9	US-10-142-419-327 Sequence 327, App
20	1992	100.0	2454	9	US-10-123-262-327 Sequence 327, App
21	1992	100.0	2454	9	US-10-142-423-327 Sequence 327, App
22	1992	100.0	2454	9	US-10-121-050-327 Sequence 327, App
23	1992	100.0	2454	9	US-10-141-755-327 Sequence 327, App
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33	1992	100.0	2454	9	US-10-124-819-327 Sequence 327, App
34	1992	100.0	2454	9	US-10-124-822-327 Sequence 327, App
35	1992	100.0	2454	9	US-10-140-925-327 Sequence 327, App
36	1992	100.0	2454	9	US-10-160-498-327 Sequence 327, App
37	1992	100.0	2454	9	US-09-944-884-1 Sequence 1, Appli
38	1992	100.0	2454	9	US-10-121-041-327 Sequence 327, App
39	1992	100.0	2454	9	US-10-121-043-327 Sequence 327, App
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45	1992	100.0	2454	9	US-10-123-910-327 Sequence 327, App

#### ALIGNMENTS

RESULT 1  
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; Sequence 1, Application US/09944413  
; Patent No. US20020156004A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548PICI  
; CURRENT APPLICATION NUMBER: US/09/944,413  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25

;; PRIOR APPLICATION NUMBER: 60/067,411  
;; PRIOR FILING DATE: December 3, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,334  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,335  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,278  
;; PRIOR FILING DATE: December 11, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,425  
;; PRIOR FILING DATE: December 12, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,696  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,694  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,702  
;; PRIOR FILING DATE: December 16, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,870  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/069,873  
;; PRIOR FILING DATE: December 17, 1997  
;; PRIOR APPLICATION NUMBER: 60/068,017  
;; PRIOR FILING DATE: December 18, 1997  
;; PRIOR APPLICATION NUMBER: 60/070,440  
;; PRIOR FILING DATE: January 5, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,086  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/074,092  
;; PRIOR FILING DATE: February 9, 1998  
;; PRIOR APPLICATION NUMBER: 60/075,945  
;; PRIOR FILING DATE: February 25, 1998  
;; PRIOR APPLICATION NUMBER: 60/112,850  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 60/113,296  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 60/146,222  
;; PRIOR FILING DATE: July 28, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US98/19330  
;; PRIOR FILING DATE: September 16, 1998  
;; PRIOR APPLICATION NUMBER: PCT/US98/23108  
;; PRIOR FILING DATE: December 1, 1998  
;; PRIOR APPLICATION NUMBER: 09/216,021  
;; PRIOR FILING DATE: December 16, 1998  
;; PRIOR APPLICATION NUMBER: 09/218,517  
;; PRIOR FILING DATE: December 22, 1998  
;; PRIOR APPLICATION NUMBER: 09/254,311  
;; PRIOR FILING DATE: March 3, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/12252  
;; PRIOR FILING DATE: June 22, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/21090  
;; PRIOR FILING DATE: September 15, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28409  
;; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28313  
;; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/28301  
;; PRIOR FILING DATE: December 1, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US99/30095  
;; PRIOR FILING DATE: December 16, 1999  
;; PRIOR APPLICATION NUMBER: PCT/US00/03565  
;; PRIOR FILING DATE: February 11, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/04414  
;; PRIOR FILING DATE: February 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/05841  
;; PRIOR FILING DATE: March 2, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/08439  
;; PRIOR FILING DATE: March 30, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/14042  
;; PRIOR FILING DATE: May 22, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/20710  
;; PRIOR FILING DATE: July 28, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US00/32678  
;; PRIOR FILING DATE: December 1, 2000  
;; PRIOR APPLICATION NUMBER: PCT/US01/06520

;; PRIOR FILING DATE: February 28, 2001

;; NUMBER OF SEQ ID NOS: 120

;; SEQ ID NO 1

;; LENGTH: 2454

;; TYPE: DNA

;; ORGANISM: Homo Sapien

US-09-944-413-1

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Score: 1992.00 Matches: 379

Percent Similarity: 100.00% Conservatives: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-09-944-413-1 (1-2454)

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Db 234 ATGAAGGAGTATGTGCTCCTATTATTCCTGGCTTTGTGCTTCTGCCAACCTTCTTTAGC 293  
Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
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Qy 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
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Qy 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80  
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Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120  
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Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
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Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260  
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Db 1314 GCAACATTCCTGTGTTTGGAGCAGATGAGTGTTCAGCTTGGGAACCTTTTGAATG 1370

RESULT 2  
US-09-944-403-1  
; Sequence 1, Application US/09944403  
; Patent No. US20020165143A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin  
; APPLICANT: Botstein, David  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gerritsen, Mary  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul  
; APPLICANT: Grimaldi, Christopher  
; APPLICANT: Gurney, Austin  
; APPLICANT: Hillan, Kenneth  
; APPLICANT: Kljavin, Ivar  
; APPLICANT: Napier, Mary  
; APPLICANT: Roy, Margaret  
; APPLICANT: Tamas, Daniel  
; APPLICANT: Wood, William  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; TITLE OF INVENTION: ACIDS ENCODING THE SAME  
; FILE REFERENCE: P2548P1C1  
; CURRENT APPLICATION NUMBER: US/09/944,403  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/866,028  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/067,411  
; PRIOR FILING DATE: December 3, 1997  
; PRIOR APPLICATION NUMBER: 60/069,334  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,335  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,278  
; PRIOR FILING DATE: December 11, 1997  
; PRIOR APPLICATION NUMBER: 60/069,425  
; PRIOR FILING DATE: December 12, 1997  
; PRIOR APPLICATION NUMBER: 60/069,696  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,694  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,702  
; PRIOR FILING DATE: December 16, 1997  
; PRIOR APPLICATION NUMBER: 60/069,870  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/069,873  
; PRIOR FILING DATE: December 17, 1997  
; PRIOR APPLICATION NUMBER: 60/068,017  
; PRIOR FILING DATE: December 18, 1997  
; PRIOR APPLICATION NUMBER: 60/070,440  
; PRIOR FILING DATE: January 5, 1998

; PRIOR APPLICATION NUMBER: 60/074,086  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/074,092  
; PRIOR FILING DATE: February 9, 1998  
; PRIOR APPLICATION NUMBER: 60/075,945  
; PRIOR FILING DATE: February 25, 1998  
; PRIOR APPLICATION NUMBER: 60/112,850  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 60/113,296  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 60/146,222  
; PRIOR FILING DATE: July 28, 1999  
; PRIOR APPLICATION NUMBER: PCT/US98/19330  
; PRIOR FILING DATE: September 16, 1998  
; PRIOR APPLICATION NUMBER: PCT/US98/25108  
; PRIOR FILING DATE: December 1, 1998  
; PRIOR APPLICATION NUMBER: 09/216,021  
; PRIOR FILING DATE: December 16, 1998  
; PRIOR APPLICATION NUMBER: 09/218,517  
; PRIOR FILING DATE: December 22, 1998  
; PRIOR APPLICATION NUMBER: 09/254,311  
; PRIOR FILING DATE: March 3, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/12252  
; PRIOR FILING DATE: June 22, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/21090  
; PRIOR FILING DATE: September 15, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28409  
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28313  
; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/28301  
; PRIOR FILING DATE: December 1, 1999  
; PRIOR APPLICATION NUMBER: PCT/US99/30095  
; PRIOR FILING DATE: December 16, 1999  
; PRIOR APPLICATION NUMBER: PCT/US00/03565  
; PRIOR FILING DATE: February 11, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/04414  
; PRIOR FILING DATE: February 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/05841  
; PRIOR FILING DATE: March 2, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/08439  
; PRIOR FILING DATE: March 30, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/14042  
; PRIOR FILING DATE: May 22, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/20710  
; PRIOR FILING DATE: July 28, 2000  
; PRIOR APPLICATION NUMBER: PCT/US00/32678  
; PRIOR FILING DATE: December 1, 2000  
; PRIOR APPLICATION NUMBER: PCT/US01/06520  
; PRIOR FILING DATE: February 28, 2001  
; NUMBER OF SEQ ID NOS: 120  
; SEQ ID NO 1  
; LENGTH: 2454  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-09-944-403-1

Alignment Scores:  
Pred. No.: 1.95e-216 Length: 2454  
Score: 1992.00 Matches: 379  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-09-944-403-1 (1-2454)

Qy 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPheSer 20  
Db 234 ATGAAGGAGTAGTGTCTCTATATCTCGGCTTGTGCTGCTGCCAACCCCTTCTTAGC 293  
Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40







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; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 1
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-944-944-1

Alignment Scores:
Pred. No.:      1.95e-216      Length:      2454
Score:          1992.00        Matches:      379
Percent Similarity: 100.00%    Conservative:  0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:      100.00%     Indels:        0
DB:               9           Gaps:          0

US-09-944-884-2 (1-379) x US-09-944-944-1 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
DB 234 ATAAGGAGATGTGCTTCTATTAATTCCTGTGCTTTGTGCTCTGCCAAACCCCTCTTTTATGC 293
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
DB 294 CCTTCACATCGCACTGAAGATATGATGCTGAAGGATATGGAAGACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
DB 414 CCAAGAAGCCATTTTTTTCATTTGATCTGTTTCCAAATGCTGTCATTTGGATGTCAGTGC 473
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
DB 474 TATTCACGAGCTGTGTACATGCTCAGATTTAGTGTTTGACCTCAGTCCCAACCAACATTC 533
QY 101 PheAspThrArgMetLeuAspLeuGluAsnAsnLysIleLysGluIleLysGluAsnAsp 120
DB 534 TTTTGATCTCGAATGCTGTGATCTTTCAAACAATAAATAAAGGAAATCAAGAAATAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnAsnLysLeuThrLysIle 140
DB 594 TTTTAAAGGACTCACTTCACCTTTATGCTGTGCTGCTGAAACACACACACAGCTTACGAGAT 653
QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
DB 654 CACCCAAAAGCCTTTCTAACACAAAAGAGTTGCGAAGGCTGTATCTGTCCACCAATCAA 713
QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
DB 714 CTAAGTGAATATCACCTTAATCTTTCCCAATCATTTAGCAGAACTCAGAAATTCATGAAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
DB 774 AAGTTTAAGAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTTACACCTTTTGCAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
DB 834 ATCAGTGCAAACCCCTCTTGTGATAATAATGGAATAGAGCCAGGGGCATTTGAAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
DB 894 GTCTTCATATCATGAAATTCAGAAAGCAAACTGACCTCAGTTCTTAAAGGCTTTACCACCA 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
DB 954 ACTTTATTGGAGCTTCATTAGATTATAATAAAATTTCAACAGTGGAACTTGAGGATTTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
DB 1014 AAACGATACAAAGAACTACAAAGGCTGGGCTTAGGAAACCAACAAATCACAGATATCGAA 1073

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281	QY	AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu	300
1074	Db	AATGGGAGTCTTGCTAACATACACCTGTGAGAGAAATACATTGGAAAAACAATAAACTA	1133
301	QY	LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer	320
1134	Db	AAAAAATCCCTTCAGATTACAGAGTTGAAATACCTCCAGATAATCTTCCTTCATTCT	1193
321	QY	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340
1194	Db	AATTCAATTGCAAGAGTGGGAGTAAATGACTCTGTGCCAAGTGCACAAAGATGAAGAA	1253
341	QY	SerLeuTyrSerAlaIleSerLeuPheAsnAspProValLysTyrTrpGluMetGlnPro	360
1254	Db	TCVTTATACAGTGCATAAGTTTATTCAACACCCTGGTGAATCTCGGAAATYGCACACT	1313
361	QY	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet	379
1314	Db	GCAACATTCGTGTGTGTTTGGACAGAAATCAGTGTTCAGCTTGGGAACATTTGGAATG	1370

## RESULT 5

US-09-944-907-1  
: Sequence 1, Application US/09944907  
: Publication No. US20020198147A1  
: GENERAL INFORMATION:  
: APPLICANT: Baker, Kevin  
: APPLICANT: Botstein, David  
: APPLICANT: Eaton, Dan  
: APPLICANT: Ferrara, Napoleone  
: APPLICANT: Filvaroff, Ellen  
: APPLICANT: Gerritsen, Mary  
: APPLICANT: Goddard, Audrey  
: APPLICANT: Godowski, Paul  
: APPLICANT: Grimaldi, Christopher  
: APPLICANT: Gurney, Austin  
: APPLICANT: Hillan, Kenneth  
: APPLICANT: Kljavin, Ivar  
: APPLICANT: Napier, Mary  
: APPLICANT: Roy, Margaret  
: APPLICANT: Tumas, Daniel  
: APPLICANT: Wood, William  
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
: TITLE OF INVENTION: ACIDS ENCODING THE SAME  
: FILE REFERENCE: P2548P1C1  
: CURRENT APPLICATION NUMBER: US/09/944, 907  
: CURRENT FILING DATE: 2001-08-31  
: PRIOR APPLICATION NUMBER: 09/866, 028  
: PRIOR FILING DATE: 2001-05-25  
: NUMBER OF SEQ ID NOS: 120  
: SEQ ID NO 1

Alignment Scores:	
Pred. No.:	1.95e-216
Score:	1992.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
	Length:
	2454
	Matches:
	379
	Conservative:
	0
	Mismatches:
	0
	Indels:
	0
	Gaps:
	0

US-09-944-884-2 (1-379) X US-09-944-907-1 (1-2454)

Qy	1	MetLys	Glu	Tyr	Val	Leu	Leu	Leu	Phe	Leu	Ala	Leu	Cys	Ser	Ala	Leu	Ala	Pro	Phe	Ser	20
Db	234	ATGAAG	GAG	TAT	GCCT	CCT	ATT	TCT	TGCT	TTTGCT	CTGCC	AAACCC	CTTC	TAT	TAC	293					
Qy	21	Pro	Ser	His	Ile	Leu	Leu	Lys	Asn	Met	Met	Leu	Lys	Asp	Met	Glu	Asp	Thr	Asp	Asp	40
Db	294	CCTT	CAC	ACAT	CTGC	ACAT	TGAA	CAAT	TAT	GCT	GGA	GGT	AT	GGA	GAC	ACAC	CAT	GAT	GAT	353	

## RESULT 6

US-09-944-929-1  
; Sequence 1, Application US/09944929  
; Publication No. US20020197612A1  
; GENERAL INFORMATION:

Db	714	CTAAGTGAATACACACTTAATCTTTCCCAAAATCATTAGCAGAACCTCAGAAATTCATGAAAAAT	
Qy	181	LysVallyLysLysIleGlnLysAspThrPhelysglyMetasnlalaLeuHisValLeuGlu	200
Db	774	AAAGTTAAGAAAATACAAAAGGACACAAATCAAAGGAATGAATGTTTTACACGTTTGGAA	833
Qy	201	MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr	220
Db	834	ATGAGTGCAAAACCCTCTTGATAATAATGGGATAGACGCCAGGGGCATTTGAAGGGGTGACG	893
Qy	221	ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro	240
Db	894	GTGTTTCCATATFACAATITGCAGAAAGCAAACTGACCTCAGTTCCCTAAAGCGTTACCA	953
Qy	241	ThrLeuLeuGluLeuHisLeuAspTyrrAsnLysIleSerThrValGluLeuGluAspPhe	260
Db	954	ACTTTATGGAGCTTCACTTAGATATTAATAAAATTTCAACAGTGGAACTTGAGGATTTT	1013
Qy	261	LysArgTyrrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu	280
Db	1014	AAACGATACAAAGAACCTACAAAGGCTGGGCTAGSAAACAACAAATACACAGATATCGAA	1073
Qy	281	AsnGlySerLeuAlaAsnIleProArgValargGluIleHisLeuGluAsnAnLysLeu	300
Db	1074	AATGGGAGTCTTGCTTAACATACCAACGCTGTGAGAGAAAATACATTTGGAAAAACAATAA	1133
Qy	301	LysLysIleProSerGlyLeuProGluLeuLysTyrrLeuGlnIleIlePheLeuHisSer	320
Db	1134	AAAAAATCCCTTCAGGATACCAGAGTTGAAATACCTCCAGATAATCTTTCCCTCATPCT	1193
Qy	321	AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys	340
Db	1194	AATTCAATGCAAGAGTGGGATTAATGACTTCTGTCCACAGTCCCAAGATGAAGAAA	1253
Qy	341	SerLeuTyrrSerAlaIleSerLeuPheAsnAsnProVallylTyrrTrpGluMetGlnPro	360
Db	1254	TCTTTATACAGTGCATAAGTTTATTCCAACAACCCGGTGAAATACTGGGAAATGCAACCT	1313
Qy	361	AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet	379
Db	1314	GCAACATTTCTGTGTGTTTTGAGCAGAAATGAGTGTTCCAGCTTGGAACTTTTGGAAATG	1370

RESULT 7  
US-10-028-072-327  
; Sequence 327, Application US/10028072  
; Publication No. US20030004311A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: DeForge, Laura  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang  
; TITLE OF INVENTION:  
; FILE REFERENCE:  
; CURRENT APPLICATION NUMBER: US/10/028,072  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/049911  
; PRIOR FILING DATE: 1997-06-18  
; PRIOR APPLICATION NUMBER: 60/056974  
; PRIOR FILING DATE: 1997-08-26

[illegible]

; PRIOR APPLICATION NUMBER: 60/088858  
 ; PRIOR FILING DATE: 19/98-06-11  
 ; PRIOR APPLICATION NUMBER: 60/089532  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089599  
 ; PRIOR FILING DATE: 1998-06-17  
 ; PRIOR APPLICATION NUMBER: 60/089907  
 ; PRIOR FILING DATE: 1998-06-18  
 ; PRIOR APPLICATION NUMBER: 60/089947  
 ; PRIOR FILING DATE: 1998-06-19  
 ; PRIOR APPLICATION NUMBER: 60/090349  
 ; PRIOR FILING DATE: 1998-06-23  
 ; PRIOR APPLICATION NUMBER: 60/090429  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090445  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090538  
 ; PRIOR FILING DATE: 1998-06-24  
 ; PRIOR APPLICATION NUMBER: 60/090863  
 ; PRIOR FILING DATE: 1998-06-26  
 ; PRIOR APPLICATION NUMBER: 60/091360  
 ; PRIOR FILING DATE: 1998-07-01  
 ; PRIOR APPLICATION NUMBER: 60/091519  
 ; PRIOR FILING DATE: 1998-07-02  
 ; PRIOR APPLICATION NUMBER: 60/091982  
 ; PRIOR FILING DATE: 1998-07-07

## Alignment Scores:

Pred. No.: 1.95e-216 Length: 2454  
 Score: 1992.00 Matches: 379  
 Percent Similarity: 100.00% Conservatives: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-028-072-327 (1-2454)

QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20  
 DB 234 ATGAAGAGTATGTGCTCTTATTCCTGCGCTTGTGCTGCGCAACCTCTTTAGC 293  
 QY 21 ProSerHisLeuLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
 DB 294 CCTTCACATCGCACTGAAGATATGATGCTGAAGGATATGAAGACACAGATGATGAT 353  
 QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
 DB 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413  
 QY 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80  
 DB 414 CCNAGAGCCATTTTTCCTATTTGATCTGTTTCCATGTTGCTGCTGCTGCTGCTGCTGCT 473  
 QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100  
 DB 474 TATTCACGAGTGTACATGCTCAGATTTAGTTTACCTCAGCTCAGCTCAGCTCAGCTCAGCT 533  
 QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLeuLysGluAsnAsp 120  
 DB 534 TTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 593  
 QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuLeuLeuAsnAsnLysLeuThrLysIle 140  
 DB 594 TTTAAGGAGTCACTTCACTTTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCT 653  
 QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgLeuTyrLeuSerHisAsnGln 160  
 DB 654 CACCAAAAGCCCTTCTAACCACAAAGAGTTCGGAAGGCTGATCTGCTCCACATCAA 713  
 QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
 DB 714 CTAAGTGAATACCACTTAATCTTCCAAATCATTTAGCAGAACTCAGAAATTCATGAAAT 773

QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200  
 DB 774 AAAGTTAAGAAATACAAAAGGACACATTCAAAAGGAATGAATGCTTTACACGTTTGGAA 833  
 QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220  
 DB 834 ATGAGTGCAAAACCTCTTGATATAATGGGATAGAGCCAGGGGCATTTGAAGGGTGACG 893  
 QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240  
 DB 894 GTGTTCCATATCAGAATTCAGAGCAAAACTGACCTCAGTTCTTAAAGGCTTACCACCA 953  
 QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuAspPhe 260  
 DB 954 ACTTATTGGAGCTTCACCTTAGATTATAATAAAATTTCAACAGTGGAACTTGAGGATTTT 1013  
 QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280  
 DB 1014 AAACGATACAAAGAACTACAAAGCTGGGCTAGGAACAACAATAATCAGATATCGAA 1073  
 QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300  
 DB 1074 AATGGGAGTCTTGCTACATACCAACCGTGTGAGAGAAATACATTTGGAAAAACAATAAACTA 1133  
 QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320  
 DB 1134 AAAAAATCCCTTCAGGATTCAGAGATTGAAATACCTCCAGATAATCTTCTCTCATCT 1193  
 QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340  
 DB 1194 AATTCATTCAGAGTGGGAGTAAATGACTTCTGCAACAGTGCACAAAGATGAAGAAA 1253  
 QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360  
 DB 1254 TCTTTATACAGTGCATAAGTTTATTCAACAACCCGGTGAATACTGGGAAATGCAACCT 1313  
 QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379  
 DB 1314 GCACATTCCTGTGTGTTTGGACAGAAATGAGTGTTCAGCTTGGGAACTTTGGAATG 1370

## RESULT 8

US-10-121-049-327  
 ; Sequence 327, Application US/10121049  
 ; Publication No. US20030022239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Beresini, Maureen  
 ; APPLICANT: DeForge, Laura  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Filvaroff, Ellen  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Gerritsen, Mary E.  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Sherwood, Steven  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Stewart, Timothy A.  
 ; APPLICANT: Tumas, Daniel  
 ; APPLICANT: Watanabe, Colin K  
 ; APPLICANT: Wood, William  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3330R1C17  
 ; CURRENT APPLICATION NUMBER: US/10/121,049  
 ; CURRENT FILING DATE: 2002-04-12  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 327  
 ; LENGTH: 2454  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien

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US-10-121-049-327
Alignment Scores:
Pred. No.: 1 95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-121-049-327 (1-2454)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAAGGAGTATGCTCTCTATTATTCCTGGCTTCTGCCAAACCCCTCTTTAGC 293
C-- 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
. 294 CCTTCACATCGCACTGAAGAAATATGCTGCAAGGATATGGAAGACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
Db 414 CCAAGAAGCCATTTTTCATTTGATCTGTTCCCAATGCTCCATTTGGATGCTCAGTGC 473
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCAGAGTGTGATATGCTCAGATTTAGGTTTGGACCTCAGTCCCAACCAATTCGA 533
QY 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLeuLysGluAsnAsp 120
Db 534 TTGTGATCTCGAATGCTGATCTTCAAAACATAAATAAATTAAGAAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140
Db 594 TTAAAGGACTCACTTCACTTTATGCTGCTGATCTGCTGATCAACCAACCAAGTAAAG 653
QY 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
Db 654 CACCCAAAAGCCVTTTCAACCAACAAAGAGTTGCGAAGGCTGTATCTGCTCCCAATCAA 713
C-- 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
. 714 CTAAGTGAATACCATCTTATCTTCCCAATCATTAGCAACTCAGAACTCATGAATAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAAGTTAAGAAATACAAAGGACACATCAAGAGGATGAATGCTTTACACGTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATCAGTGAACCCCTCTTGATATAATATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db 894 GTGTTCCATATCAGAAATTCAGAAAGCAAACTGACCTCAGTTCCTTAAAGGCTTACCACCA 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTGGAGCTTCACCTTAGATTAATAATAAATTTCAACAGTGAAGCTTGAGGATTTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 ARAAGTACAAGAACTACAAAGGCTGGGCTTAGGAACAAACAAATCACAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300
Db 1074 AATGGGAGTCTTCTAATCAATACCAACGCTGTGAGAGAAATACATTTGGAAACAACTAA 1133
QY 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGlnIleIlePheLeuHisSer 320
```

```
Db 1134 AAAAAATCCCTTCAGGATTACAGAGTTGAATACCTCCAGATAATCTTCTTCATTCT 1193
QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCAAATTCGAAGAGTGGAGTAAATGACTTCTGTCCAACAGTCCCAAGATGAAGAA 1253
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db 1254 TCTTTATACAGTCAATAAGTTTATTCACAACACCCGGTGAAATACTGGGAATGCAACT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTTTCGTTGTTTGTGAGCAGAATGAGTGTTCAGCTTGGGAACCTTGGAAATG 1370

RESULT 9
US-10-123-904-327
; Sequence 327, Application US/10123904
; Publication No. US20030022328A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; TITLE OF INVENTION: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330R1C54
; CURRENT APPLICATION NUMBER: US/10/123,904
; CURRENT FILING DATE: 2002-04-16
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-123-904-327
Alignment Scores:
Pred. No.: 1 95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-123-904-327 (1-2454)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAAGGAGTATGCTCTCTATTATTCCTGGCTTCTGCCAAACCCCTCTTTAGC 293
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
Db 294 CCTTCACATCGCACTGAAGAAATATGCTGCAAGGATATGGAAGACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80
```

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Db 414 CCAGAGCCATTTTTCATTTGATCTGTCCCAATGTCTCAATTTGGATGTCAAGTC 473
Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCAGAGCTTGTACATCTGCTCAGATTTAGTTGACCTCAGTCCCAACCAACATTC 533
Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysGluAsnAsp 120
Db 534 TTTGATACCTCGAATGCTGTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGAT 593
Qy 121 PheLysGlyLeuThrSerLeuThrGlyLeuLysLeuAsnAsnLysLysLeuThrLysIle 140
Db 594 TTTAAGGACTCACTTCACCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Qy 141 HisProLysAlaPheLeuThrLysLysLeuArgGlyLeuThrLysLysLeuThrLysIle 160
Db 654 CACCAAAAGCCCTTCTAACCAACAAGAGCTTGCAGAGGCTGATCTGTCTCCCAACATCAA 713
Qy 161 LeuSerGluLysLeuProLysSerLeuLysLeuLysLeuLysLeuLysLeuLysLeu 180
Db 714 CTAAGTGAATACCACTTAATCTTCCCAATATATTAGCAGAACTCAGAAATTCATGAAT 773
Qy 181 LysValLysLysLysGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAGTTAAGAAATACAAAGGACACATTCAGAGGAAATGATGCTTTACAGCTTTTGAA 833
Qy 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTCAAAACCTCTGTGATAATATGATGATAGAGCAGGGGCTTTGAAGGGGTGACG 893
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db 894 GTGTTCCATATACAAATGTGAGAGCAAGCAAACTGACCTTCAATGAAGCTTTACCAACA 953
Qy 241 ThrLeuLeuGluLeuHisLeuAspThrAsnLysLysLysLysLysLysLysLysLysLys 260
Db 954 ACTTATGAGGCTTCACTAGATATATATATATATATATATATATATATATATATATAT 1013
Qy 261 LysArgThrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysLysLysLysLysLys 280
Db 1014 AAACGATACAAAGCACTACAAAGCTGGGCTAGGAAACAACAATAATCAGATATCGAA 1073
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluLysLeuGluAsnAsnLysLeu 300
Db 1074 AATGGGAGCTTGTCTACATACCACTGCTGAGAGAAATACATTTGGAAAAACAATAACTA 1133
Qy 301 LysLysLysProSerGlyLeuProGluLeuLysThrLeuGlnLysLysLysLysLysLys 320
Db 1134 AAAAAATCCCTTCAGAGATACCAAGCTTCAAAATACCTCCAGATAATCTTCCCTTCATCT 1193
Qy 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCATTCAGAGTGGGAGTAAATGACTTCTGTCCACAGTGCACAAAGATGAAGAAA 1253
Qy 341 SerLeuThrSerLysLysLeuPheAsnAsnProValLysThrTrpGluMetGlnPro 360
Db 1254 TCCTTATACAGTGCATAAATTTTATTCACAAACCCGCTGAAATCTGGGAAATGCAACCT 1313
Qy 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLysGlyAsnPheGlyMet 379
Db 1314 GCACATTTCTGTGTGTTTGACAGAAATGAGTGTTCAGCTTGGGAACCTTTGGAATG 1370
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## RESULT 10

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US-10-140-470-327
; Sequence 327, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
```

```
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3330RIC160
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; LENGTH: 2454
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-140-470-327

Alignment Scores:
Pred. No.: 1,95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 0

US-09-944-884-2 (1-379) x US-10-140-470-327 (1-2454)

Qy 1 MetLysGluThrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAGGAGTATGTGCTCTCTATTTATTCCTGGCTTTGTCTCTCCAAACCTTCTTTAGC 293
Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40
Db 294 CTTTCACATCCACTGAGAAATATGATGCTCAAGATATGCAAGATATGCAAGACACAGATGAT 353
Qy 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
Qy 61 ProArgSerHisPhePheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80
Db 414 CCAAGAGGCAATTTTTCATTTGATCTGTTTCCAAATGTGCTCAATTTGGATGTCAAGTC 473
Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCAGAGTGTACATTCCTCAGATTTAGGTTTGACCTCAGTCCCAACCAACATTC 533
Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluLysGluAsnAsp 120
Db 534 TTTGATACCTCGAATGCTGTGATCTTCAAAACAATAAAATTAAGGAAATCAAGAAATGAT 593
Qy 121 PheLysGlyLeuThrSerLeuThrGlyLeuLysLeuAsnAsnLysLysLeuThrLysIle 140
Db 594 TTTAAGGACTCACTTCACCTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653
Qy 141 HisProLysAlaPheLeuThrLysLysLeuArgGlyLeuThrLysLysLeuThrLysIle 160
Db 654 CACCAAAAGCCCTTCTAACCAACAAGAGTTCGAGAGGCTGATCTGTCTCCCAACATCAA 713
Qy 161 LeuSerGluLysLeuProLysSerLeuLysLeuLysLeuLysLeuLysLeuLysLeu 180
Db 714 CTAAGTGAATACCACTTAATCTTCCCAATATATTAGCAGAACTCAGAAATTCATGAAT 773
Qy 181 LysValLysLysLysGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
```



Db 774 AAGTTAAGAAATACAAAAGGACACATTCAAAGGAATCAATGCTTTACACGTTTGGAA 833  
Qy 201 MetSerAlaAsnProLeuAspAsnGlyIleGluProGlyAlaPheGluGlyValThr 220  
Db 834 ATGAGTGAACCCCTCTTGATTAATGAGTAGAGCCAGGGGCAATTTGAAGGGGTGAGC 893  
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240  
Db 894 GTGTTCCATATCAGAAATGCAGAACAAACCTGACCTCAGTTCCCTAAAGGCTTACCACCA 953  
Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260  
Db 954 ACTTTATTGGAGCTTCACCTAGATTATATAAATTTCAACAGTGGAACTTGAGGATTTT 1013  
Qy 261 LysArgTyrLysGluLeuGluArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280  
Db 1014 AARCATACAAGAACTACAAGGCTGGCCCTAGGAACAACAATAACAGATATCGAA 1073  
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300  
Db 1074 AATGGAGCTCTGTACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAATA 1133  
Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGluIleIlePheLeuHisSer 320  
Db 1134 AAAAAATCCCTTCAGGATTACACAGATTGAAATACCTCCAGATAATCTTCTTCATTCT 1193  
Qy 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340  
Db 1194 AATCAATGTCAAGAGTGGGAGTAATGACTCTGTCCACAGTGCACCAAGATGAAGAA 1253  
Qy 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360  
Db 1254 TCTTTATACAGTCAATAAGTTTATTCAACACCCGGTGAAATCTGCGGAAATGCAACCT 1313  
Qy 361 AlathrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379  
Db 1314 GCAACATTCTGTTGTTGTGACGAGAAATGAGTGTGACCTTGGGAACTTTGGAAATG 1370

## RESULT 11

US-10-175-746-327  
; Sequence 327, Application US/10175746  
; Publication No. US20030027270A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Beresini, Maureen  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Sherwood, Steven  
; APPLICANT: Smith, Victoria  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K  
; APPLICANT: Wood, William  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3330R1C353  
; CURRENT FILING DATE: 2002-06-19  
; Prior Application removed - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 550  
; SEQ ID NO 327  
; LENGTH: 2454  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
US-10-175-746-327

## Alignment Scores:

Pred. No.: 1.95e-216 Length: 2454  
Score: 1992.00 Matches: 379  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0  
US-09-944-884-2 (1-379) x US-10-175-746-327 (1-2454)  
Qy 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20  
Db 234 ATGAAGAGTAGTAGCTCTCTATTATCTGCTTGTGCTCTGCCAAACCCCTCTTTTACG 293  
Qy 21 ProSerHisIleAlaLeuLysAsnMetMetLeuLysAspMetGluAspThrAspAsp 40  
Db 294 CCTTCACACATCGCACTGCAAGAAATATGATGCTGAAGGATATGGAAGACACAGATGAT 353  
Qy 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413  
Qy 61 ProArgSerHisPhePhePhePhePhePhePhePhePhePhePhePhePhePhePhe 80  
Db 414 CCAAGAAGCCCATTTTTCCTATTTGATCTGTTCCTATGTTGCTGCTGCTGCTGCTGCT 473  
Qy 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100  
Db 474 TATTCACAGCTGTACATGCTCAGATTTAGTTTGACCTCAGTCCCAACCAACATTC 533  
Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnLysIleLysGluIleLysGluAsnAsp 120  
Db 534 TTTGATACTCGAATGCTTGTCTTCAAAACAATAAATAAGGAAATCAAGAAATGAT 593  
Qy 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140  
Db 594 TTTAAAGGACCTCACCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 653  
Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160  
Db 654 CACCCAAAAGCCCTTCTTACCAACAAAGAGTTGCGAAGCTGTATCTGCTCCCAACAA 713  
Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
Db 714 CTAAGTGAATACCACTTAATCTTCCCAATCATTAGCAGAACTCAGAAATTCATGAAAT 773  
Qy 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200  
Db 774 AAAGTTAAGAAATACAAAGGACACATTCAAAGGAATGAATGCTTTACACGTTTGGAA 833  
Qy 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220  
Db 834 ATGAGTGAACCCCTCTTGATTAATGAGTAGAGCCAGGGGCAATTTGAAGGGGTGAGC 893  
Qy 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuPro 240  
Db 894 GTGTTCCATATCAGAAATGCAGAACAAACCTGACCTCAGTTCCCTAAAGGCTTACCACCA 953  
Qy 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260  
Db 954 ACTTTATTGGAGCTTCACCTAGATTATATAAATTTCAACAGTGGAACTTGAGGATTTT 1013  
Qy 261 LysArgTyrLysGluLeuGluArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280  
Db 1014 AARCATACAAGAACTACAAGGCTGGCCCTAGGAACAACAATAACAGATATCGAA 1073  
Qy 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300  
Db 1074 AATGGAGCTCTGTACATACCACGCTGTGAGAGAAATACATTTGGAAACAATAAATA 1133  
Qy 301 LysLysIleProSerGlyLeuProGluLeuLysTyrLeuGluIleIlePheLeuHisSer 320  
Db 1134 AAAAAATCCCTTCAGGATTACACAGATTGAAATACCTCCAGATAATCTTCTTCATTCT 1193

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QY 321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db 1194 AATTCAAATTCGACAGTGGAGTAATGACTTCTCTCCCAACAGTGCCAAAGATGAAGAAA 1253
QY 341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db 1254 TCTTTATACAGTGCATAGATTTATTCACACACCCGGTGAATATCTGGGAATGCAACCT 1313
QY 361 AlaThrPheArgCysValLeuSerArgMetSerValGlnLeuGlyAsnPheGlyMet 379
Db 1314 GCAACATTTTCGTTGTCTTTTGACGAGATGAGTGTTCAGCTGGGAACCTTTGGAATG 1370
RESULT 13
US-10-176-918-327
; Sequence 327, Application US/10176918
; Publication No. US20030027275A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330R1C382
; CURRENT APPLICATION NUMBER: US/10/176,918
; CURRENT FILING DATE: 2002-06-20
; Prior Application removed - See File wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 327
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-176-918-327
Alignment Scores:
Pred. No.: 1,95e-216 Length: 2454
Score: 1992.00 Matches: 379
Percent Similarity: 100.00% Conservative: 0
c Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
US-09-944-884-2 (1-379) x US-10-176-918-327 (1-2454)
QY 1 MetLysGluTyrValLeuLeuLeuPheLeuAlaLeuCysSerAlaLysProPhePheSer 20
Db 234 ATGAAGAGATGTGCTCTCTATTTATTCCTGGCTTGTGCTCTGCCAAACCCCTCTTTAC 293
QY 21 ProSerHisIleAlaLeuLysAsnMetMetLysLysAspMetGluAspThrAspAsp 40
Db 294 CCTTCACATCGCACTGAAGAATATGATGCTGAAGATATGAAGACACACAGATGATGAT 353
QY 41 AspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60
Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413
QY 61 ProArgSerHisPhePheProPhePheProMetCysProPheGlyCysGlnCys 80
Db 414 CCAGAGAGCCATTTTTTTCATTTGATCTGTTTCCCAATGTGTCATTTGATGATGATGATGAT 473
```

```
QY 81 TyrSerArgValValHisCysSerAspLeuGlyLeuThrSerValProThrAsnIlePro 100
Db 474 TATTCACAGATGTGTACATTTGCTCAGATTTAGTGTTCACCTCAGTCCCAACCAACATTTCCA 533
QY 101 PheAspThrArgMetLeuAsnAsnLysIleLysLysLysLysLysLysLysLysLys 120
Db 534 TTTGATACCTCGAATGCTTGTGATCTTCAAAACATAAAATTAAGGAAATCAAGAAATGAT 593
QY 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnAsnLysLeuThrLysIle 140
Db 594 TTTAAAGGACTCACTTCATCTTATGCTGTGATCTCTGATCTCTCAACAACAACAAGCTTAACGAAGATT 653
QY 141 HisProLysAlaPheLeuThrLysLysLysLeuArgLeuLeuSerHisAsnGln 160
Db 654 CACCCCAAAAGCCCTTCTTAACCAAAAAGAGTTCGGAAGGCTGTATCTGTCCCAACATCAA 713
QY 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180
Db 714 CTAAGTGAATACCACTTAACTTCCCAATCATTAGCAGAACTCAGAAATTCATGAAT 773
QY 181 LysValLysLysIleGlnLysAspThrPheLysGlyMetAsnAlaLeuHisValLeuGlu 200
Db 774 AAAGTTAAGAAAATACAAAAGGACACATTCAAAGGAATGAATGCTTTACACGCTTTTGGAA 833
QY 201 MetSerAlaAsnProLeuAspAsnAsnGlyIleGluProGlyAlaPheGluGlyValThr 220
Db 834 ATGAGTGCAACCCCTCTTATATAATGGATAGAGCCAGGGGCATTTGAAGGGGTGACG 893
QY 221 ValPheHisIleArgIleAlaGluAlaLysLeuThrSerValProLysGlyLeuProPro 240
Db 894 GGTGTCATATCAGAATTCAGAGAGCAAAACCTGACCTCAGTCTCTAAAGGCTTTACCACT 953
QY 241 ThrLeuLeuGluLeuHisLeuAspTyrAsnLysIleSerThrValGluLeuGluAspPhe 260
Db 954 ACTTTATTGGAGCTTCACCTTAGATTTATAATAAATTTCAACAGTGGAACTTTGAGGATTT 1013
QY 261 LysArgTyrLysGluLeuGlnArgLeuGlyLeuGlyAsnAsnLysIleThrAspIleGlu 280
Db 1014 AAACGATACAAAAGAACTACAAAAGCTGGGCCTAGGAAACAACAATAATCAGATATCGAA 1073
QY 281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnAsnLysLeu 300
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US-10-176-921-327
; Sequence 327, Application US/10176921
; Publication No. US20030027276A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
```

; APPLICANT: Goddard,Audrey  
 ; APPLICANT: Godowski,Paul J.  
 ; APPLICANT: Gurney,Austin L.  
 ; APPLICANT: Sherwood,Steven  
 ; APPLICANT: Smith,Victoria  
 ; APPLICANT: Stewart,Timothy A.  
 ; APPLICANT: Tumas,Daniel  
 ; APPLICANT: Watanabe,Colin K  
 ; APPLICANT: Wood,William  
 ; APPLICANT: Zhang,Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; FILE REFERENCE: P3330R1C288  
 ; CURRENT APPLICATION NUMBER: US/10/176,921  
 ; PRIOR FILING DATE: 2002-06-20  
 ; NUMBER OF SEQ ID NOS: 550  
 ; SEQ ID NO 327  
 ; LENGTH: 2454  
 ; TYPE: DNA  
 ; ORGANISM: Homo Sapien  
 US-10-176-921-327

Alignment Scores:  
 Pred. No.: 1,95e-216 Length: 2454  
 Score: 1992.00 Matches: 379  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 9 Gaps: 0

US-09-944-884-2 (1-379) x US-10-176-921-327 (1-2454)  
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 Db 294 CCTTCACATCGCACTGAAGAATAATGATGCTGAAGGATATGGAAGACACAGATGATCAT 353  
 Qy 41 AspAspAspAspAspAspAspAspAspGluAspAsnSerLeuPheProThrArgGlu 60  
 Db 354 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 413  
 Qy 61 ProArgSerHisPheProPheAspLeuPheProMetCysProPheGlyCysGlnCys 80  
 Db 414 CCAAGAAGCCATTTTTTCCATTTGATCTGTTTCCAAATGTCCTCAATTTGGATGTCAGTGC 473  
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 Qy 101 PheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120  
 Db 534 TTTGTAFACTCGATGCTTGTCTTCAAACAATAAATAAAGGAAATCAAGAAAATGAT 593  
 Qy 121 PheLysGlyLeuThrSerLeuTyrGlyLeuIleLeuAsnAsnLysLeuThrLysIle 140  
 Db 594 TTTAAAGGACTCACTTCATTTATGTCGTGATGCTGGAACAACAACAAGCTAACGAAGATT 653  
 Qy 141 HisProLysAlaPheLeuThrThrLysLysLeuArgGluLeuTyrLeuSerHisAsnGln 160  
 Db 654 CACCACCAAGCCCTTCTACACACAGAAGTTGCCAAGGCTGTATCTGTCCCAACATCAA 713  
 Qy 161 LeuSerGluIleProLeuAsnLeuProLysSerLeuAlaGluLeuArgIleHisGluAsn 180  
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Mon Jun 2 10:28:59 2003

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QY pheAspThrArgMetLeuAspLeuGlnAsnAsnLysIleLysGluIleLysGluAsnAsp 120
Db |||||||
534 TTGTGACTCGAATGCTTGAATCTCAAAACACATAAATTAAGGAAATCAAGAAATGAT 593
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Db |||||||
594 TTTAAGGACTCACCTTCACTTTATGCTGTGATCTCTGAACACAAACAAAGCTAACGAGATT 653
QY |||||||
141 HisProLysAlaPheLeuThrThrLysLysLeuArgArgLeuTyrLeuSerHisAsnGln 160
Db |||||||
654 CACCCAAAAGCCCTTTTAAACCAAGAAAGTTGCGAAGGCTGTACTCTGCCACAAATCAA 713
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Db |||||||
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QY |||||||
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Db |||||||
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QY |||||||
281 AsnGlySerLeuAlaAsnIleProArgValArgGluIleHisLeuGluAsnLysLeu 300
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QY |||||||
321 AsnSerIleAlaArgValGlyValAsnAspPheCysProThrValProLysMetLysLys 340
Db |||||||
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QY |||||||
341 SerLeuTyrSerAlaIleSerLeuPheAsnAsnProValLysTyrTrpGluMetGlnPro 360
Db |||||||
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QY |||||||
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Job time : 217 secs